

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2003, 01:51:30 ; Search time 80 Seconds
(without alignments)

710.301 Million cell updates/sec

Title: US-09-868-547-4

Perfect score: 1886

Sequence: 1 MASLNNRKAKEIFQCAL.....FQYKISPTFGYLSLIEIYP 358

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1886	100.0	358	21	AAV96584
2	1012	53.7	350	21	AAV96587
3	1012	53.7	351	21	AAV96585
4	1006	53.3	348	21	AAV96586
5	997	52.9	350	21	AAV96583
6	636.5	33.7	347	20	AAV24396
7	590.5	31.3	375	20	AAV05661
8	580.5	30.8	350	20	AAV27183
9	567	30.1	370	20	AAV05662
					Glycine max isofla
					Glycine max isofla
					Glycine max isofla
					Glycine max partia
					Coptis japonica no
					Maize caffeic O-me
					(S)-3'-hydroxy-N-m
					Maize caffeic O-me

10 540.5 28.7 366 20 AAY05663
11 527 27.9 368 21 AAG40137
12 527 27.9 382 21 AAG40136
13 527 27.9 382 23 ABB93248
14 521 27.6 368 21 AAG28589
15 521 27.6 382 21 AAG28588
16 521 27.6 383 21 AAG28587
17 485 25.7 325 21 AAG31303
18 485 25.7 325 23 ABB93247
19 435 23.1 354 20 AAY05660
20 434 23.0 296 21 AAG40138
21 426 22.6 363 20 AAY43041
22 392.5 20.8 253 21 AAG31304
23 390.5 20.7 330 21 AAG25274
24 390.5 20.7 330 21 AAG25598
25 390.5 20.7 330 21 AAG47428
26 390.5 20.7 340 21 AAG25597
27 390.5 20.7 340 21 AAG47427
28 390.5 20.7 363 21 AAG25596
29 390.5 20.7 363 21 AAG47426
30 390.5 20.7 363 23 ABB93811
31 390.5 20.7 364 14 AAR34764
32 379.5 20.1 365 15 AAR63203
33 379.5 20.1 365 22 AAE12021
34 376.5 20.0 316 21 AAG25275
35 375.5 19.9 222 21 AAG31305
36 371.5 19.7 364 14 AAR34762
37 371.5 19.7 365 20 AAY01133
38 371.5 19.7 365 23 AAU00015
39 369.5 19.6 365 19 AAW84132
40 367.5 19.5 314 14 AAR34763
41 367 19.5 371 23 AAE16516
42 365 19.4 368 19 AAW84128
43 364.5 19.3 309 21 AAG25276
44 364.5 19.3 365 23 AAE16510
45 362 19.2 368 24 AAE29785

ALIGNMENTS

RESULT 1

AAV96584

ID AAY96584 standard; Protein; 358 AA.

XX

AC AAY96584;

XX

DT 26-SBP-2000 (first entry)

XX

DE Glycine max isoflavone O-methyltransferase.

XX

KW Isoflavone O-methyltransferase; soybean; degradation; daidzein;

KW Flavonoid; flower colour; growth; pollination; irradiation.

XX

OS Glycine max.

XX

PN WO200037656-A2.

XX

PD 29-JUN-2000.

XX

PF 20-DEC-1999; 99WO-US30338.

XX

PR 21-DEC-1998; 98US-0113190.

XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX

PI Famodu OO, McGonigle B, Odell JT, Fader GM, Falco SC;

XX

DR WPI; 2000-442680/38.

XX

PT N-PSDB; AAA29322.

XX

PT New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries

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XX PS Claim 10; Page 32-33; 39pp; English.
XX PA
XX PI
XX PI Famoou OO, McGonigle B, Odell JT, Fader GM, Falco SC;
XX DR WPI; 2000-442680/38.
XX DR N-PSDB; AAA29325.
XX PT New polynucleotide encoding flavonoid biosynthetic enzymes for creating
XX PT transgenic plants and for immunological screening of cDNA libraries
XX PS Claim 10; Page 37-39; 39pp; English.
XX CC AA96583-87 are (partial) isoflavone O-methyltransferases isolated from
XX CC various soybean (Glycine max) tissues. cDNA libraries se4, srl, srlc
XX CC and sslic were prepared from soybean embryo (19 days after flowering),
XX CC root, 8-day old root and seed (25 days after flowering).
XX CC Isoflavone O-methyltransferase catalyses the first step in degradation
XX CC of daidzein. Suppression of this enzyme will yield higher concentrations
XX CC of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
XX CC co-pigments in flower colour, stimulate pollen tube growth, attract
XX CC pollinators, act as feeding deterrents and protect against UV
XX CC irradiation in fruits and seeds. The cDNA and proteins can be used to
XX CC isolate homologues, for immunological screening and for positive
XX CC selection methods.
XX SQ Sequence 358 AA;
XX Query Match 100.0%; Score 1886; DB 21; Length 358;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-189;
XX Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 MASSLNNGRKASEIFQGOALLYKHLGFTDSKCLKMWVELDIPDIHSHSGQPTPSEL 60
XX Db 1 MASSLNNGRKASEIFQGOALLYKHLGFTDSKCLKMWVELDIPDIHSHSGQPTPSEL 60
XX QY 61 VSILQVPTKTRQVOSLMRYLAHNGFEEIVRTHDNIEAYALTAASELLVKSSELSAPMV 120
XX Db 61 VSILQVPTKTRQVOSLMRYLAHNGFEEIVRTHDNIEAYALTAASELLVKSSELSAPMV 120
XX QY 121 EYFLEPNCQGANLQKRWVHEEDLTVFEVSLGTPFWDINKDPAYKSFNEAMACDSQML 180
XX Db 121 EYFLEPNCQGANLQKRWVHEEDLTVFEVSLGTPFWDINKDPAYKSFNEAMACDSQML 180
XX QY 181 NLAPDCNWNVEGLESIVDVGGGTGITAIIICEAPPKLCMWLERPNVVENLSGSNNLTF 240
XX Db 181 NLAPDCNWNVEGLESIVDVGGGTGITAIIICEAPPKLCMWLERPNVVENLSGSNNLTF 240
XX QY 241 VGGDMFKCIPKADAVLLKLVHNNNDNCKILENCKEASGESKTGKVVVDITVINENK 300
XX Db 241 VGGDMFKCIPKADAVLLKLVHNNNDNCKILENCKEASGESKTGKVVVDITVINENK 300
XX QY 301 DERQVTELKLMVHMACIINGKERKEEDWKLFMEAGFQSKYKISPPFTGYLSLIEIYP 358
XX Db 301 DERQVTELKLMVHMACIINGKERKEEDWKLFMEAGFQSKYKISPPFTGYLSLIEIYP 358
XX RESULT 2
XX AA96587
XX ID AA96587 standard; Protein; 350 AA.
XX AC AA96587;
XX XX
XX DT 26-SEP-2000 (first entry)
XX XX
XX DE Glycine max isoflavone O-methyltransferase.
XX KW Isoflavone O-methyltransferase; soybean; degradation; daidzein;
XX KW Flavonoid; flower colour; growth; pollination; irradiation.
XX OS Glycine max.
XX FH Key Location/Qualifiers
XX FT Misc-difference 89
XX FT /note= "Encoded by GAAGATCATGAA"
XX PN WO200037656-A2.
XX XX
XX PD 29-JUN-2000.
XX XX
XX PF 20-DEC-1999; 99WO-US30338.
XX XX
XX PR 21-DEC-1998; 98US-0113190.

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XX XX (DUFO ) DU PONT DE NEMOURS & CO E I.
XX PA
XX PI
XX PI Famoou OO, McGonigle B, Odell JT, Fader GM, Falco SC;
XX DR WPI; 2000-442680/38.
XX DR N-PSDB; AAA29325.
XX PT New polynucleotide encoding flavonoid biosynthetic enzymes for creating
XX PT transgenic plants and for immunological screening of cDNA libraries
XX PS Claim 10; Page 37-39; 39pp; English.
XX CC AA96583-87 are (partial) isoflavone O-methyltransferases isolated from
XX CC various soybean (Glycine max) tissues. cDNA libraries se4, srl, srlc
XX CC and sslic were prepared from soybean embryo (19 days after flowering),
XX CC root, 8-day old root and seed (25 days after flowering).
XX CC Isoflavone O-methyltransferase catalyses the first step in degradation
XX CC of daidzein. Suppression of this enzyme will yield higher concentrations
XX CC of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
XX CC co-pigments in flower colour, stimulate pollen tube growth, attract
XX CC pollinators, act as feeding deterrents and protect against UV
XX CC irradiation in fruits and seeds. The cDNA and proteins can be used to
XX CC isolate homologues, for immunological screening and for positive
XX CC selection methods.
XX SQ Sequence 350 AA;
XX Query Match 53.7%; Score 1012; DB 21; Length 350;
XX Best Local Similarity 54.9%; Pred. No. 2.4e-97;
XX Matches 196; Conservative 69; Mismatches 84; Indels 8; Gaps 5;
XX QY 3 SSLNNGRKASEIFQGOALLYKHLGFTDSKCLKMWVELDIPDIHSHSGQPTPSELVS 62
XX Db 1 ASMN-OKETELFEGQSLLYMQLVHLRPMCLKWAVOLGIPDIQNH- KPISLSDLS 57
XX QY 63 ILOVPTKTRQVOSLMRYLAHNGFEEIVRTHDNIE-AYALTAASELLVKSSELSAPMV 121
XX Db 58 TLQPPNANAFVQRFMEFLAHNGIFE---IHSELTALTAPASKLLVNSDCLSPMV 114
XX QY 122 YFLEPNCQGANLQKRWVHEEDLTVFEVSLGTPFWDINKDPAYKSFNEAMACDSQMLN 181
XX Db 115 AFTDPLRNKVVHHLGEWIRGEDSVFTANGTSAWGLEKNPEYFSLFNEAMADSRVD 174
XX QY 182 LAFRDCNWNVEGLESIVDVGGGTGITAIIICEAPPKLCMWLERPNVVENLSGSNNLTFV 241
XX Db 175 LALKNCTSVFEGLDSDVDVGGGTGTARIICDAFPKLCVVDLPVHVNLTGTNNLSFV 234
XX QY 242 GDMFKCIPKADAVLLKLVHNNNDNCKILENCKEASGESKTGKVVVDITVINENK 301
XX Db 235 GGMFNSIFORDAVLLKLVHNNNDNCKILENCKEASGESKTGKVVVDITVINENK 294
XX QY 302 ERQVTELKLMVHMACIINGKERKEEDWKLFMEAGFQSKYKISPPFTGYLSLIEIYP 358
XX Db 295 DEDMTOTKLSLDIIM-LTWNGRTERTEKWKLFMEAGFQSKYKISPPFTGYLSLIEIYP 350
XX RESULT 3
XX AA96585
XX ID AA96585 standard; Protein; 351 AA.
XX AC AA96585;
XX XX
XX DT 26-SEP-2000 (first entry)
XX XX
XX DE Glycine max isoflavone O-methyltransferase.
XX KW Isoflavone O-methyltransferase; soybean; degradation; daidzein;
XX KW Flavonoid; flower colour; growth; pollination; irradiation.
XX OS Glycine max.
XX FH Key Location/Qualifiers

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FT Misc-difference 90
XX /note= "Encoded by GAAGATCATGAA"
XX
XX WO200037656-A2.
XX
XX 29-JUN-2000.
XX
XX 20-DEC-1999; 99WO-US30338.
XX
XX 21-DEC-1998; 98US-0113190.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Famodu OO, McGonigle B, Odell JT, Fader GM, Falco SC;
XX
XX WPI; 2000-442680/38.
XX
XX N-PSDB; AAA29323.
XX
XX New polynucleotide encoding flavonoid biosynthetic enzymes for creating
XX transgenic plants and for immunological screening of cDNA libraries
XX
XX Claim 10; Page 34-35; 39pp; English.
XX
XX AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from
XX various soybean (Glycine max) tissues. cDNA libraries se4, srl, srlc
XX and sllc were prepared from soybean embryo (19 days after flowering),
XX root, 8-day old root and seed (25 days after flowering).
XX
XX Isoflavone O-methyltransferase catalyses the first step in degradation
XX of daidzein. Suppression of this enzyme will yield higher concentrations
XX of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
XX co-pigments in flower colour, stimulate pollen tube growth, attract
XX pollinators, act as feeding deterrents and protect against UV
XX irradiation in fruits and seeds. The cDNA and proteins can be used to
XX isolate homologues, for immunological screening and for positive
XX selection methods.
XX
XX Sequence 351 AA;
XX
XX
XX Query Match 53.7%; Score 1012; DB 21; Length 351;
XX Best Local Similarity 54.9%; Pred. No. 2.4e-97;
XX Matches 196; Conservative 69; Mismatches 84; Indels 8; Gaps 5;
XX
XX QY 3 SSLNNGKASEIFQGOALLYKHLGFTDSKCLKMWVELDIPDIHSHGQPTTFSELVS 62
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 2 ASMN- QKTELFEGOSLLYMLYGLHRLPMCLKWAVOLGIPDIIONHA--KPISLSLVS 58
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 63 ILQVPTKTRQVOSLMRYLAHNGFFPIVRTHDNIE-AVALTAASELLYKSSLSLAPMVE 121
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 59 TLQIPANAAVQVRFWRFLAHNGIFE--IHESQELTYALTPAKULLVNSSDHCLSPMVL 115
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 122 YLEPNCQGANWOLKRWVHEEDLTVPFVSLGTFPWDFINKDPAYNKSFNEMACDSOMLN 181
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 116 AFTDPLRNKVKYHHLGEWIRGEDPSVETAHTGTSANGGLEKNPEYFSLFNEAMASDSRVD 175
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 182 LAPRDCNWPEGLSIVDVGGGTGTAKIICEAPPKLKCWLPRNPVVENLSSGNLTFV 241
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XX 176 LALKNCTSVPEGLDSMVDVGGGTGTARIICDAFPKLCVVDLPVHVENLTCTNNLSFV 235
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 242 GGMFMKICPKADAVLLKVLHNWVNDNCKILENCKEALSGESKTKGVVVDIVINENKD 301
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 236 GGMFNSIFQADAVLLKVLHNWVNDNCKILQKCRDSISSKNSGKVIIDAVINERKLD 295
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 302 EROVTEKLMVDVHMACIINGKREKEDWKLFMEAGFQSYKISPTGVLSLIEIYP 358
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 296 DPMQTKLSLDIIM-LTYNGRTERTEKEWKQLFIEAGFKYKIFPIFGFRSLIEIYP 351
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX
XX RESULT 4
XX AAY96586
XX ID AAY96586 standard; Protein; 348 AA.
XX
XX AC AAY96586;
XX

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DT 26-SEP-2000 (first entry)
XX
XX Glycine max partial isoflavone O-methyltransferase.
XX
XX Isoflavone O-methyltransferase; soybean; degradation; daidzein;
XX Flavonoid; flower colour; growth; pollination; irradiation.
XX
XX Glycine max.
XX
XX WO200037656-A2.
XX
XX 29-JUN-2000.
XX
XX 20-DEC-1999; 99WO-US30338.
XX
XX 21-DEC-1998; 98US-0113190.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Famodu OO, McGonigle B, Odell JT, Fader GM, Falco SC;
XX
XX WPI; 2000-442680/38.
XX
XX N-PSDB; AAA29324.
XX
XX New polynucleotide encoding flavonoid biosynthetic enzymes for creating
XX transgenic plants and for immunological screening of cDNA libraries
XX
XX Claim 10; Page 35-36; 39pp; English.
XX
XX AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from
XX various soybean (Glycine max) tissues. cDNA libraries se4, srl, srlc
XX and sllc were prepared from soybean embryo (19 days after flowering),
XX root, 8-day old root and seed (25 days after flowering).
XX
XX Isoflavone O-methyltransferase catalyses the first step in degradation
XX of daidzein. Suppression of this enzyme will yield higher concentrations
XX of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
XX co-pigments in flower colour, stimulate pollen tube growth, attract
XX pollinators, act as feeding deterrents and protect against UV
XX irradiation in fruits and seeds. The cDNA and proteins can be used to
XX isolate homologues, for immunological screening and for positive
XX selection methods.
XX
XX Sequence 348 AA;
XX
XX Query Match 53.3%; Score 1006; DB 21; Length 348;
XX Best Local Similarity 54.7%; Pred. No. 1e-96;
XX Matches 192; Conservative 64; Mismatches 91; Indels 4; Gaps 3;
XX
XX QY 9 RKASEIFQGOALLYKHLGFTDSKCLKMWVELDIPDIHSHGQPTTFSELVSILQVP 68
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 1 QKAMELFEGOSLLYMLYGLHRLPMCLKWAVOLGIPDIIONHA--KPIITSLDVLSTLIQPP 58
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 69 TTRQVOSLMRYLAHNGFFPIVRTHDNIE-AVALTAASELLYKSSLSLAPMVEYLEPN 127
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 59 SKAGFVQPMFLAHNGIPDIRESQDDHELAVALTPASKLLVSCDHCLSPMVRNMTDPL 118
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 128 CQGANWOLKRWVHEEDLTVPFVSLGTFPWDFINKDPAYNKSFNEMACDSOMLNLAFRDC 187
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 119 LMTTHFFGEWIRGEDPTVHETAFGTSPWGLEKNPTQMSLFNEAMASDSRMVDLAKNC 178
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 188 NMVFEGLSIVDVGGGTGTAKIICEAPPKLKCWLPRNPVVENLSSGNLTFVGGDMFK 247
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 179 TSVFEGLSMVDVGGGTGTARIICEAPPKLKCWLPRNPVVENLSSGNLTFVGGDMFN 238
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 248 CTPKADAVLLKVLHNWVNDNCKILENCKEALSGESKTKGVVVDIVINENKDERQVTE 307
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 239 SFFQTDVALLKVLHNWVNDNCKILKCKKDSISSKNGRGKVIIDIIINEKLDPMTR 298
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 308 LKLLMDVHMACIINGKREKEDWKLFMEAGFQSYKISPTGVLSLIEIYP 358
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX 299 TKLSLDIVMS-TMNGRERSEKWKQMFIEAGFQHCKIFPIFGFRSLIEIYP 348
XX :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
XX

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Qy 306 TELKILMDVHMACININGKRRKEDWKLFWEAGFQSKISPTGYLSLIEIYP 350
 Db 299 TRTKLSLDIVMS--TWNGRERSEKWKQMPFEAGFKHCKIFFPGFRSLIEIYP 350

 RESULT 6
 AAY24396
 ID AAY24396 standard; Protein; 347 AA.
 XX
 XX AAY24396;
 XX
 XX 20-SEP-1999 (first entry)
 XX
 XX Coptis japonica norcoclaurine 6-O-methyltransferase.
 DE
 XX Coptis japonica; norcoclaurine 6-O-methyltransferase; 6-OMT;
 KW secondary metabolite; coclaurine; reticuline.
 XX
 XX Coptis japonica.
 XX
 XX JP111178577-A.
 XX
 XX 06-JUL-1999.
 PD
 XX 24-DEC-1997; 97JP-0355045.
 PF
 XX 24-DEC-1997; 97JP-0355045.
 PR
 XX (MITC) MITSUI PETROCHEM IND CO LTD.
 PA
 XX WPI; 1999-437310/37.
 DR
 XX N-PSDB; AAX90136.
 XX
 XX New norcoclaurine 6-O-methyl-transferase - useful for preparation
 PT of secondory plant metabolite
 PT
 XX Claim 1; Page 11-12; 27pp; Japanese.
 XX
 XX The present sequence represents norcoclaurine 6-O-methyltransferase
 CC (6-OMT). Also described is a method for the preparation of the sec
 CC ondary metabolite of a plant derived from coclaurine or reticuline.
 CC
 XX Sequence 347 AA;
 SQ

 Query Match 33.7%; Score 636.5; DB 20; Length 347;
 Best Local Similarity 38.9%; Pred. No. 7.3e-58;
 Matches 133; Conservative 70; Mismatches 132; Indels 7; Gaps 0

 Qy 18 QALLYKHLGFDISKCLWMVLDIPDIHSHSHGQPTFSELVSLQVPPTKTRQVW
 Db 11 QAKLWNFIYGFASLVLKCAVQLDLANII--HNSGTSMTLSELSSRLPSQPVNEDAL
 Qy 78 MYLHANGFFEIVRHIDNIEAYALTAASELLVKSSLSLAPWVEYFLPNCQGANQV
 Db 69 MYLVHMKLFTKASIDGELR-YGLAPPAXLYLKGWDKCMVGSILAITDKDFNAPWYH
 Qy 138 WHEEDLTVFVSLGTPFDWDFINKDPAYNKSFNEAMACDSQMLNAP-RDCNWVFEG
 Db 128 GLSGSGTAFAEKALGTNIWGMVAEHPKXNQLFNEAMANDSRLIMSAVKCEGNIENG
 Qy 197 IVDVGGGTGITAKITCEAPPKLKMVLRRPNVNLGSSNNLTFVGGDMFKCIPKAD
 Db 188 IVDVGGGTGTAVRNITANAFPHIKCTVYDLPVHIDSPGYSEVHCVAGDMFKFIPKAD
 Qy 257 LKLVLHNWNDNDCKILNCKEAISSGSKTGKVVVIDTVINENKDERQVTELKILMD
 Db 248 MKCILHDDWDKCEIILKCEKAV--PVKGGKVIIVDVLNV-QSEHYPTKMRLLD
 Qy 317 ACINGKRRKEDWKLFWEAGFQSKISPTGYLSLIEIYP 358
 Db 305 MLNTGGKERTBEENKLLHIDAGYKGHKITQTAVOSVIEAYP 346

Qy	11	ASEIFQOALLYKHLGLFDSDCKLWVLDLPDIHSHSHGQPIITFSELVSLIQVPPTK	70
Db	9	SODLQADHLLHSLCFKSLALAVDLRIPDAIHGGAG-GATLLQIAETALPESK	67
Qy	71	TRQVOSLMRYLAHNGFFEIVR-----IH-----DNIEAYALTAASELLVKS--SE	113
Db	68	LKALRLRLVLTGTGIFSVVEQPPAGGGDDSVHTSDDEAVVVYRLTAASFLVSDDVST	127
Qy	16	OQOALLYKHLGLFDSDCKLWVLDLPDIHSHSHGQPIITFSELVSLIQVPPTKTRQV	75
Db	13	KAQAHWKKIYGFADSLVLRCAVELGVIDIINN--OPMALADLASKLPVSDVNCNLY	70
Qy	76	SLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSPAPVVEFLEPNCOGANNOL	135

Db 71 RILRLVLRKMEILRVEKSDGKKYALEPIATLLSNKRSVPMILGTMQDFMTPWHS 130
 QY 136 KRWHEDLTVPFVSLGTPFDWDFINKDPAYNKSFNEMACDSQMLNLFAP----RDCNWVF 191
 Db 131 KDGLSDNG-HAFKANGMTIWEYLEGHDPQSQLFNEGMAGETRLTLTSSLISGRD---MF 186
 QY 192 EGLSIVDVGSGTGITAKIICEAFPKLKMVLERPNVVENSGSNLTFVGGDMFKCIPK 251
 Db 187 QQIDSLVDVGGNGTIVKASDAFPHIKCTFDLPHVIANSDLEPNIRIGDMFKSVPS 246
 QY 252 ADAVLLKLVHNDNDCKILENCKEASIGESKTKGVVVIDTVINENKDERQVTELKLL 311
 Db 247 AQAILKILHWDNEDSILKQCRNAVPRDG--GKVIIVDVALDESD-HELSSTRLI 303
 QY 312 MDVEMACIINGKEREKEDWKLFMEAGFQSYKISPTGTGLSLIETYP 358
 Db 304 LDIDMLVNTGKERTKEVWEKIVKSAGFGCKIRHIAAQSVIEVFP 350

RESULT 9

AA05662
 ID AA05662 standard; Protein; 370 AA.

AC AA05662;

DT 19-JUL-1999 (first entry)

DE Maize caffeic O-methyltransferase.

KW Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant.

OS Zea mays.

PN WO9910498-A2.

PD 04-MAR-1999.

PF 24-AUG-1998; 98WO-US17519.

PR 12-MAY-1998; 98US-0076851.

PR 27-AUG-1997; 97US-0057082.

PA (PION-) PIONEER HI-BRED INT INC.

PI Bowen BA, Helentjaris TG, Wang X;

DR WPI; 1999-204667/17.

DR N-PSDB; AAX25201.

XX Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis

PS Claim 9; Page 95-96; 166pp; English.

CC The present sequence is a caffeic O-methyltransferase of maize, encoded by a clone (see AAX25201) isolated from a line A632 library. The invention provides methods and compositions relating to altering lignin biosynthesis and/or the lignin composition of plants. Isolated nucleic acids (see AAX25196-216) that code for proteins (see AA05657-77) involved in lignin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (especially maize or sorghum), and transgenic plants and seeds. The claimed nucleic acids can be used to transform a plant to modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lignin biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as chemical feedstock. Plant material of increased lignin content can be used as a fuel source, and in the pulp and paper industry. Decreased lignin content

CC improves the digestibility of fodder crops.

SQ Sequence 370 AA;

Query Match 30.18; Score 567; DB 20; Length 370;
 Best Local Similarity 34.78; Pred. No. 1.7e-50;

Matches 137; Conservative 64; Mismatches 132; Indels 62; Gaps 11;

QY 1 MASSLNGRKASHIFQOALLYKHLGFIDSKLKNMVELDIPDIHSHSGOPITFSEL 60

Db 1 MALMQESSQODMLQAHDELHLSLCAKSLALTVALDLRIPDAIHGCG--ATLLQI 58

QY 61 VSILOVPTTKRQVQSLMRVLAHNGFPEIVRIH-----DNIEA---YALTAASELLVK- 110

Db 59 LAETGLHPSKLRALRLRLRVLTVTGTFS-VQVOQPPAGSDDEAVVYVRLTAASRFLVSD 117

QY 111 --SSELSLAPMVEYFLEPNCG-----AWNQLKR-----WVHEEDLT 145

Db 118 EVSTATTLAFVSLALQPIAASPHALGICAWFQEHPSYGLAFROTPTLWEHADDV- 176

QY 146 VFEVSLGTPFDWDFINKDPAYNKSFNEMACDSQ-MLNLAFRDCNWVFEGLSIVDVGGGT 204

Db 177 -----NALLNKGWADSRFLMPEIVLRQCGEMFRGINSLVGVGGH 216

QY 205 GITAKIICEAFPKLKMVLERPNVVENSGSNLTFVGGDMFKCIPKADAVLLKLVHNV 264

Db 217 GGAATAAIAAAPPVHKCSVLDPHVAGAPSDGVQFVAGNMFESIPPATAVFLKKTLDW 276

QY 265 NDNDCKILENCKEASIGESKTKGVVVIDTVINENKDERQVTELKLLMDVHMACIINGKE 324

Db 277 GDECVKILNCKQAIPPRDAGKVIIDVVGVKQSNIKHQETQVWFDLYMVA-VNGVE 335

QY 325 RXBEDWKKLFMEAGFQSYKISPTGTGLS-LRIETYP 358

Db 336 RDEQWKKIPAEAGFKYKILPVIGDVSVIIEVVP 370

RESULT 10

AA05663

ID AA05663 standard; Protein; 366 AA.

AC AA05663;

DT 19-JUL-1999 (first entry)

DE Maize caffeic O-methyltransferase.

KW Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant.

OS Zea mays.

PN WO9910498-A2.

PD 04-MAR-1999.

PF 24-AUG-1998; 98WO-US17519.

PR 12-MAY-1998; 98US-0076851.

PR 27-AUG-1997; 97US-0057082.

PA (PION-) PIONEER HI-BRED INT INC.

PI Bowen BA, Helentjaris TG, Wang X;

DR WPI; 1999-204667/17.

DR N-PSDB; AAX25202.

XX Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis

PS Claim 9; Page 96-97; 166pp; English.

CC The present sequence is a caffeic O-methyltransferase of maize,


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PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
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PR 02-AUG-1999; 99US-0146388.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162142.

Query Match 27.9%; Score 527; DB 21; Length 368;
Best Local Similarity 34.1%; Pred. No. 2.6e-46;
Matches 126; Conservative 70; Mismatches 151; Indels 22; Gaps 10;

Qy 6 NNGRKA-SEIFOGQALYKHLGFDISKCLKMWVLDIPDIIHSHSHGQPIITFSELVIL 64
Db 3 DNKKVLDEAKASLDWKYVFGPADIAAKCAIDLKXPEAIENHPSSQPVTLAELSSAV 62
Qy 65 QVPPTKTQVQSLMRYLAHNGFFFEIVRIHONI-BAYALTAASE--LLVKSELAPWVE 121
Db 63 SASPSHLRRI--MRFLVHQGIFKEIFTKDGLATGYVNTPLSRRLMTRRDGKSLAPVL 119
Qy 122 YFLEPNCQGANQLKRW----VHEEDLTVFEVSLGTFPWFDPINKDPAYNKSFNEMACDS 177
Db 120 FETPEMLAPWLRSLSSVSSPVANGSTPPFPDAVHGKDVNSFPAQNPFLSDMINEAMACDA 179
Qy 178 -QMLNLAFCRCNVVFEGLSEIVDVGGGTGITAKIICAFPKLKCWLERNVVENLGSN 236
Db 180 RRVVPRVAGACHGLFDGVTWVDVGGGTGTMGLVKVEFPWIKGFNFDLPHVIEVAVLD 239
Qy 237 NLTFVGGDMFKCIPKADAVLLKLVLHNNDNDCKMILENCKEAKISGESKTKGVVIVDTVI 296
Db 240 GVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKLKNCKEAV--PPNIGKVLIVESVI 297
Qy 297 NENK-----DER--QVTELKLMND-VHMACIINGKREKEDWKKLFMEAGFQYKKSPT 348
Db 298 GENKTMIVDERDEKLEHVLMLDMVMMAHTSTGKERTLKEWDFVLKEAGFARYEVDRID 357
Qy 349 GYLSLIEIY 357
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RESULT 12
AAG40136

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Query Match 27.6%; Score 521; DB 21; Length 368;
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AC AAG28588;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-MAR-1999; 99US-0126264.
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PR 01-APR-1999; 99US-0127482.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
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PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.

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Title: US-09-868-547-4

Perfect score: 1886

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	376.5	20.0	364	2	US-08-204-288-5
4	371.5	19.7	365	2	US-08-715-325-2
5	367	19.5	371	4	US-09-500-569-16
6	364.5	19.3	365	4	US-09-500-569-16
7	357	18.9	358	4	US-09-500-569-4
8	350.5	18.6	368	3	US-08-991-677-6
9	338.5	17.9	354	4	US-09-500-569-12
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23	214	11.3	188	4	US-09-500-569-8
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30 189.5 10.0 621 3 US-09-382-027-1 Sequence 1, Appli
31 186.5 9.9 115 4 US-09-266-965-3 Sequence 3, Appli
32 135.5 7.2 368 4 US-09-252-991A-20452 Sequence 20452, A
33 134.5 7.1 139 4 US-09-252-991A-20476 Sequence 20476, A
34 122.5 6.5 231 4 US-09-500-569-20 Sequence 20, Appli
35 120.5 6.4 117 4 US-09-266-965-5 Sequence 5, Appli
36 119 6.3 94 1 US-08-266-45B-20 Sequence 20, Appli
37 119 6.3 94 2 US-08-748-725-20 Sequence 20, Appli
38 110.5 5.9 115 4 US-09-266-965-4 Sequence 4, Appli
39 98.5 5.2 1890 4 US-09-004-838-88 Sequence 88, Appli
40 98 5.2 541 2 US-08-540-804-16 Sequence 16, Appli
41 98 5.2 541 2 US-08-218-265-16 Sequence 16, Appli
42 98 5.2 541 3 US-08-521-872-16 Sequence 16, Appli
43 98 5.2 541 3 US-08-590-399-16 Sequence 16, Appli
44 97.5 5.2 983 2 US-08-449-645A-21 Sequence 21, Appli
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ALIGNMENTS

RESULT 1

US-08-845-742-2
; Sequence 2, Application US/08845742C
; Patent No. 5973229

GENERAL INFORMATION:

; APPLICANT: Walton, Jonathan D
; APPLICANT: Scott-Craig, John S
; TITLE OF INVENTION: Gene Encoding Herbicide Safener Binding Protein
; FILE REFERENCE: 6550-000007
; CURRENT APPLICATION NUMBER: US/08/845,742C
; CURRENT FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 363
; TYPE: PPT
; ORGANISM: Zea mays
US-08-845-742-2

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Best Local Similarity 31.4%; Pred. No. 9.2e-36;
Matches 116; Conservative 70; Mismatches 144; Indels 40; Gaps 10;

QY 12 SEIFQQAALYKHLGLFIDSKLKMVELDIPDIHSHSHGQPIITFSELVSILOVPPTKT 71
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QY 72 ROVQSLMYLAHNGFFIVIRIHDNIEAYALTAASELLV-----KSSLSLAPMVEY 122
Db 69 PFLRLRLLAASGVFTVDKOSSEERYISPVSYLLVDGIPHEDHNMHTALVLTCTSTR 128
QY 123 FLEPNCQAGMNLKRWVHE-----BDL---TVFEVSLGTPFWDINKDPAYNKSFNEA 172
Db 129 YIE-----AGUGLAENFKRDVWTPPELHCATLHFHSMG-----SLDDPFDHMASEA 176
QY 173 M-ACDSQMLNLAFRDCNNWFEGLESIVDVGGTGIT--AKIICEAFFPKLKMVLERNPV 229
Db 177 LDAHNFGEIATKREFRDLFEGIQSMTYCCGNFGDDKGARAIKVAIPHIKCTVLAPKII 236
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Db 237 ATPADGAMINYVEGDMFSPFIPPAQTIVLKLVLHLHLLDEECVKLLAQCRKAIPSRKDGK 296
QY 289 VVVIDTIVINEKDERQVTEKLLMDVHMCI INKGRKEEDWKLEFWEAGFQSYKISPT 348
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QY 349 GYLSLIEIYIP 358
Db 354 GARVAFEVYP 363

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259 LVLHNWDCMKILENCKEABGESKTKGVVIDTVINENKDERQVTEKLKLMVDVHM-A 311
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266 WICHNDGDEHCLFLKNCYEALEPA---NGKVIABCEILPEADPTSLATKNTVHVIVMLA 322
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318 CIINGKKEEDKKKLFMEAGFOSYKISPTCYLSLIEI 356
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RESULT 3
US-08-204-288-2
; Sequence 2, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
; APPLICANT: VAN DOORSSELAERE, Jan
; APPLICANT: FRITIG, Bernard J.M.
; APPLICANT: INZE, Dirk G.
; APPLICANT: JOUANIN, Lise
; APPLICANT: KNIGHT, Mary E.
; APPLICANT: VAN MONTAGU, Marc
; APPLICANT: LEGRAND, Michel
; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,288
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9119279.9
; FILING DATE: 10-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01460
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-204-288-2

Query Match 20.0%; Score 376.5; DB 2; Length 364;
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Matches 98; Conservative 69; Mismatches 136; Indels 19; Gaps 8

QY 34 LKMWELDIPILIIHSHGQPTISELSVLISQVPPKTR-----QVOSLWRYLAHNGFEEI 89
Db 36 LKATLELLIMAKAGGAPLSTSEASHL---PTKNPDAPVMDRIELLSASIL-I 91

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Db	36	LKSAVENJOLLEMAKAGPAAISSELSAQAUSTONPEAPVMDLRLLASYSVNLCTLR	95	
QY	89	IVRIHDNIEAYALTAASBELLVKSSE--LSLAEMVBYFLEPNCQGANQ----	LKRWVHHEED	143
Db	96	TLPDSSVERLYSLAPVCKYLTKNADGVSVAELL-----	LMNQDKVLMESSWYHLKD	145
QY	144	LTV-----FVYSLGTPTPWFDFINKDPAYNKSNEAMACDSQMLNIAFRDCNWPFGLSIV	198	
Db	146	AVLDGGITPFNKAYGMTAFVYHGTDTPFRNKFVNFRGMSDHSHTSMKKILLEDYKGFEGLSIN	205	
QY	199	DVGGGTGITAKIIIEAPFKLKMVLERNVVENISGGNNLTFFVGDDMPFKCIPKADAVILLK	258	

QY 187 CNWVFEGLSIVDVGGGTGTAIIICEAPFKLKWLERPNVVENLGSNNLTFVGGDMF 246
Db 196 TYKFGELGSLVDVGGGTGAHLNMIATKYPMIKGINFDLPVIEBAPSPYGVHVGDMF 255
QY 247 KCIKPADAVLLKVLVHNDNDCKMILENCKEKAISGESKTKGVVDTVINENKDERQVT 306
Db 256 VSVPGDAIPMKWICHDSDEHCLFKKCYEAL---PTNGKVILAECLLPVAPDASLPT 312
QY 307 ELKLMVDVHM-ACTINGKERKEEDWKLPMFAGFQSYKISPTGY 350
Db 313 KAVVHIDVIMLAHNPCKERTKEFEALAKAGAGFGRVVASCA 357

RESULT 9
US-09-500-569-12
; Sequence 12, Application US/09500569
; Patent No. 6329204
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; FILE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; CURRENT APPLICATION NUMBER: US/09/500,569
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,587
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Glycine max
US-09-500-569-12

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Best Local Similarity 26.4%; Pred. No. 1.1e-26;
Matches 89; Conservative 74; Mismatches 147; Indels 27; Gaps 8;
QY 38 VELDPIIHSKQPIITFSELSVLQVPPKTRQ----VQSLMRYLAHNGFFVIRIH 93
Db 27 IELGIFDIIAKAGEKASAKDIAAKL---PCKNSEGATMLDRILRLVCHSIIDCTVVA 83
QY 94 DNIEA-----YALTAASLLVK-SGELSAPMVEYFLEBNCQGANOLKRWHEEDL 144
Db 84 DOQHGPPLHOLFVYANPVAKYFASIDGASGLPLMLVLTQKALHSHWYQKDALEGGI 143
QY 145 TVFEVSLGTPWFDFINKDPAYNKSNEAMACDSQMLNLAFRDCNWNVFEGLSIVDVGGGT 204
Db 144 PFNRVH-GKHVFEYSDMNSFNQLFMAAMTNRAATLIMKKIVESYKGFELNSLVDVGGGL 202
QY 205 GITAKICEAPFKLKWLERPNVVENLGSNNLTFVGGDMFKCTPKADAVLLKVLVHND 264
Db 203 GVTNIVTSKYPHNGINFDLPVIEHASTPGVEHVGDMFSPVQGDAILMCMCLVDW 262
QY 265 NNDCKMILENCKEKAISGESKTKGVVDTVI---NENKDERQVTELKLMVDVHMCAII 320
Db 263 SDWCLKVLKNCYASIPSD---GKVIIVDGIPLPEPKTGTGASKSISQFDVLM---MTNP 316
QY 321 NKERKEEDWKLPMFAGFQSYKISPTGYLSLBIY 357
Db 317 GKRSEREEFALAKAGAGYSGIRFTCFVSDLMWMEFF 353

RESULT 10
US-08-204-288-7
; Sequence 7, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
; APPLICANT: VAN DOORSELAERE, Jan
; APPLICANT: FRITIG, Bernard J.M.
; APPLICANT: INZE, Dirk G.

APPLICANT: JOUANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-288-7

Query Match 17.9%; Score 337; DB 2; Length 365;
Best Local Similarity 27.5%; Pred. No. 1.6e-26;
Matches 96; Conservative 76; Mismatches 131; Indels 46; Gaps 12;
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Db 25 LLSSSVLPFV---LHSTIQLEVFEL-AKSNDTKLSASQIVS--QIPNCKNPDAATMLD 77
QY 76 SLMRYLAHNGFF--EIVRIHND---IEAYALTAASLLVKSS-LSLAPMVEYFLEPNC 128
Db 78 RMLVVLASYSLFTCSIIVEDENNGQKRVGLSOVGFVVRDEDCASGPLLALLOKVP 137
QY 129 QGANQKRWVHEEDLTVFEVSLGTFP-----WDFINKDPAYNKSNEAMACDSQM 179
Db 138 INSWFELKDAVLEG-----GVPDFRVHGVVHAPEPKSDPKFNDVFNKAMINHTV 188
QY 180 LNLAFRCNWNVFEGLSIVDVGGGTGTAIIICEAPFKLKWLERPNVVENLGSNNLT 239
Db 189 VMKKILENYKGFENLKTLDVGGGLGVNLKMTISKYPTIKGTNFDLPHVYVQHAPSPYGV 248
QY 240 FVGGDMFKCTPKADAVLLKVLVHNDNDCKMILENCKEKAISGESKTKGVVDTVINEN 299
Db 249 HVGDMFPSPVPGDAIPMKWILHDSHNLKLNKCYKAL---PDNGKVIIVVEAILPVK 305
QY 300 KDERQ-----VTELKLMVDVHMCAIIINGKERKEEDWKLPMFAGFQSYKI 344
Db 306 PDIDTAVVGSQCDLIM---MAQNPGKRSERSEEFRALATEAGFKGVNL 351

[illegible]

QY 258 KLVLHNNNDCKMILENCKEALSGESKTKGVVVIDTVINENKDERQVTELKLLMDVHMA 317
DB 279 KMILEMONDEDIKILKNCHOAL---PDNGKVIABEIVLPTIPDLAQATARYPPQMD--MI 333
QY 318 CIIN---GKERKEEDMKLFMEAGF 339
DB 334 MLSNRGGKERTLEFAKLATDSGF 358

RESULT 14
US-08-186-833-4
; Sequence 4, Application US/08186833
; Patent No. 5583324
; GENERAL INFORMATION:
; APPLICANT: Tarczynski, Mitchell C.
; APPLICANT: Jensen, Richard G.
; APPLICANT: Bohnert, Hans J.
; TITLE OF INVENTION: Transgenic Plants With Enhanced Mannitol
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word, Version #5.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,833
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/07/871,416
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 9221490026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-186-833-4

Query Match 16.1%; Score 303; DB 1; Length 365;
Best Local Similarity 26.5%; Pred. No. 5.4e-23;
Matches 89; Conservative 61; Mismatches 138; Indels 48; Gaps 9;

QY 34 LKMWVELDIPDIHSHSGQPIITFSELVSILOVP-PTKTROVQSLMRYLAHNGPFEIVRI 92
DB 38 LKSAFELKILDIIFSKAGGVFVSTSEIASQIGAKNPAPVLDRLMLRLASHS----- 90
QY 93 HDNTEAYALTAASELLVKSSE--LSLAPMWYFLEPNCGGAWNQL-----KRWVH 140
DB 91 -----VLTCKLQKGGGSRVYGPALCNLYLASNDGQSLGPLLVLLHDKWMMESWFH 143
QY 141 EEDLTVEVSLGTFP-----WDFINKDPAYKSFNEAMACDSQMLNLAFRDCNWWFEG 192
DB 144 LND-----YILEGGVPPKRAHGMIQDYTGTDERFNEFVFNQGMHAHTILVMKKLLDNYNGFN 200
QY 193 GLESTVDVGGGTGTAKIICEAFPKLKMVLERPNVVENLSSNNLTFVGGDMFKCIPKA 252
DB 201 DVKVLVDVGGNIGVNVIVAKHTIKGINIDYLDLPHVIADAFSPGVEHVGGMFESIPQA 260

QY 253 DAVLLKLVLHNNNDCKMILENCKEALSGESKTKGVVVIDTVI---NENKDERQVTEL 308
DB 261 DAIFMKVWLHDSHCHVKILNKCYESL---AKGKIILVESLIPVPEDNLESHMVFSL 317
QY 309 KLLMDVHMACINGKERKEEDMKLFMEAGFOSYKI 344
DB 318 DCHTLVHNQ---GGKERSKEDFEALASKTGFTVDV 350

RESULT 15

US-09-615-192A-274
; Sequence 274, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 274
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-615-192A-274

Query Match 15.0%; Score 283.5; DB 4; Length 328;
Best Local Similarity 28.0%; Pred. No. 4.8e-21;
Matches 79; Conservative 50; Mismatches 142; Indels 11; Gaps 4;

QY 34 LKMWVELDIPDIHSHSGQPIITFSELVSILOVP-PTKTROVQSLMRYLAHNGPFEIVRI 92
DB 53 LKVHVELGILELL---AKGDQLSPLDIVARLSIDNPAAPDTIDRLMLRLASYSILSCTLV 109
QY 93 HDN---IEAYALTAASELLVKSSELSLAPMWYFLEPNCGGAWNQLKRWVHEEDLTVE 148
DB 110 EDKGRFORLYGLGPRSKFFLDQNGASTPLTHMLLQELTLECNWCLKDAVKEGGADPFT 169
QY 149 VSLGTFPWFDFINKDPAYKSFNEAMACDSQMLNLAFRDCNWWFEGLESIVDVGGGTGITA 208
DB 170 RRHGMVFDYMGQDPREFNDLYNKSMTGSAIYMPKIAQHYEGFSKAKTVVNVGGIGETL 229
QY 209 KIICEAFPKLKMVLERPNVVENLSSNNLTFVGGDMFKCIPKADAVLLKLVLHNNND 268
DB 230 KTLISKNPHIRAINYDLPHVIATAPPFGITHVGGDILKSVFKADVHFLKSVLHRGDDEF 289
QY 269 CMKILENCKEALSGESKTKGVVVIDTVINENKDERQVTELKL 310
DB 290 CVKVLKNWEAL---PPTGKVIIVEVTPEYPTGDDVDSQTTL 328

Search completed: November 10, 2003, 03:22:41
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2003, 03:21:21 ; Search time 76 Seconds
(without alignments)
809.030 Million cell updates/sec

Title: US-09-868-547-4

Perfect score: 186

Sequence: 1 MASSLNNGKASEIFQOAL.....FQYKISPTGYSILRIYP 358

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	590.5	31.3	375	12	US-10-361-460-5
2	567	30.1	370	12	US-10-361-460-6
3	540.5	28.7	366	12	US-10-361-460-7
4	435	23.1	354	12	US-10-361-460-4
5	371.5	19.7	365	10	US-09-947-027-6
6	371.5	19.7	365	14	US-10-091-009-6
7	350.5	18.6	368	9	US-09-796-256A-6
8	337.5	17.9	360	12	US-10-289-757-103
9	331.5	17.6	360	12	US-10-289-757-102
10	331.5	17.6	360	12	US-10-289-757-182
11	329.5	17.5	361	12	US-10-289-757-105
12	328.5	17.4	360	12	US-10-289-757-104
13	293	15.5	375	15	US-10-213-473-29
14	283.5	15.0	328	16	US-10-174-693-274
15	273.5	14.5	351	12	US-09-953-348-133

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16 273.5 14.5 351 15 US-10-267-255-133 Sequence 133, Appl
17 258.5 13.7 160 16 US-10-174-693-275 Sequence 275, App
18 227.5 12.1 156 16 US-10-174-693-272 Sequence 272, App
19 225.5 12.0 331 15 US-10-156-761-10380 Sequence 10380, A
20 213.5 11.3 285 12 US-09-769-734-15 Sequence 15, Appl
21 202 10.7 145 16 US-10-174-693-270 Sequence 270, App
22 190.5 10.1 359 15 US-10-156-761-9919 Sequence 9919, Ap
23 186.5 9.9 115 12 US-09-953-348-3 Sequence 3, Appli
24 186.5 9.9 115 15 US-10-267-255-3 Sequence 3, Appli
25 186.5 9.9 115 15 US-10-267-255-3 Sequence 3, Appli
26 121.5 6.4 133 15 US-10-267-849-38 Sequence 38, Appl
27 120.5 6.4 117 12 US-09-953-348-5 Sequence 5, Appli
28 120.5 6.4 117 15 US-10-267-255-5 Sequence 5, Appli
29 110.5 5.9 115 12 US-09-953-348-4 Sequence 4, Appli
30 110.5 5.9 115 12 US-10-267-255-4 Sequence 4, Appli
31 103.5 5.5 347 15 US-10-166-087-38 Sequence 38, Appli
32 98 5.2 555 10 US-09-801-368-350 Sequence 350, App
33 97.5 5.2 983 10 US-09-771-161A-227 Sequence 227, App
34 97.5 5.2 983 12 US-10-345-680-2 Sequence 2, Appli
35 97.5 5.2 983 15 US-10-205-823-97 Sequence 97, Appli
36 96.5 5.1 459 9 US-09-815-242-12703 Sequence 12703, A
37 96.5 5.1 952 15 US-10-216-556-2 Sequence 2, Appli
38 93.5 5.0 993 11 US-09-823-187-39 Sequence 39, Appli
39 93.5 5.0 993 11 US-09-823-187-41 Sequence 41, Appli
40 93.5 5.0 998 11 US-09-823-187-40 Sequence 40, Appli
41 93.5 5.0 998 11 US-09-823-187-42 Sequence 42, Appli
42 93.5 5.0 998 11 US-09-823-187-43 Sequence 43, Appli
43 93.5 5.0 1033 9 US-09-888-615-75 Sequence 75, Appli
44 92.5 4.9 841 9 US-09-861-451A-30 Sequence 30, Appli
45 90.5 4.8 821 12 US-10-205-219-11 Sequence 11, Appl

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ALIGNMENTS

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RESULT 1
US-10-361-460-5
; Sequence 5, Application US/10361460
; Publication No. US20030163839A1
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
; TITLE OF INVENTION: Biosynthesis and Uses thereof
; FILE REFERENCE: 0709
; CURRENT APPLICATION NUMBER: US/10/361,460
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/057,082
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays
US-10-361-460-5

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Query Match 31.3%; Score 590.5; DB 12; Length 375;
Best Local Similarity 37.3%; Pred. No. 7.3e-52;
Matches 139; Conservative 62; Mismatches 141; Indels 31; Gaps 12;

QY 11 ASBIFQOALLYKHLGCFIDSKLKNWVELDIPDIHSHSHGQPIFSELVSILOVPTK 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 SQDLLQDSELHHSJCFAXSLALAVDLRIPDAIHHCAG-GATLLQLALETALPESK 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 TROVQSLMRVLAHNGPFEIVR-----IH-----DNIEAYALTAASELLVKS--SE 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 LRALRLRLRVLTIGFVSVVEQPPAGGGDDSTVHTSDDEAVVVVRLTAARFLVDDVST 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 LSIAPMVEYFLEP--NCQGANOLKRWVHEEDLTFEVSIG---TP-FWDFINKDPAYNK 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 ATLAPFVSLAQPIAACPHALG-ISAWFROEQHEPSPYGLAFRTPTIWEHADD---VNA 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 168 SFNEAMACDSQ-MLNLAFRDCNWVFEGLSIVDVGSGTGITAKIICEAPFKLKCWLRLP 226
Db 184 LNKGNWADSRFLMPVILRECGTTFGIDSLVDVGGHGAATAAAPHUKCSVLDP 243
QY 227 NVVENLGSNNLTFVGGDMFKCIPKADAVLLKLVLHNDNDCKMILENCKEKAISGESKT 286
Db 244 HVVAGAPSDGNVQFVAGNMFESIPPTAVFLKTLHDGDDCEVKILNCKQAISPRDAG 303
QY 287 GKVVVITVINENKDERQVTELKLMVHMVACIINGKERKEDWKLFBVAGFQSKISP 346
Db 304 GKVIILDVVVGKQSNIKHQETQVMPDLYMA-VNGVERDEQEWKKIETGAGFKDYKILP 362
QY 347 FTGYLS-LIEIYP 358
Db 363 VIGDVSIIIEVYP 375

RESULT 2
US-10-361-460-6
; Sequence 6, Application US/10361460
; Publication No. US20030163839A1
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
; FILE REFERENCE: 0709
; CURRENT APPLICATION NUMBER: US/10/361,460
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/057,082
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Zea mays
US-10-361-460-6

Query Match 30.1%; Score 567; DB 12; Length 370;
Best Local Similarity 34.7%; Pred. No. 1.8e-49;
Matches 137; Conservative 64; Mismatches 132; Indels 62; Gaps 11;

QY 1 MASSLNNGRKASEIFQGOALLYKHLGLFIDSKLKMVVELDIPDIHSHSHGQPIITFSEL 60
Db 1 VALMQESSQDQMLQAHDELHSLCFKSLALVALDLRIPDAIHGGG--ATLLQI 58
QY 61 VSIQVPTKTRQVOSLMRYLAHNGFFEIVRIH-----DNIEA---VALTAASLLLVK- 110
Db 59 LAETGLHPSKLRALRLMRVLTVTGTF--VQVQPPAGSDDEAVVYVRLTAASRFLVSD 117
QY 111 --SSELSAPVVEYLENCOG-----ANNQLK-----WHEEDLT 145
Db 118 EVSTATLAPFVSLALQTAASPHALGTCAMFRQEHFSPYGLAFROTPTLWEHADVV- 176
QY 146 VFEVSLGTGTFWDFINKDPAYNKSFNEMACDSQ-MLNLAFRDCNWVFEGLSIVDVGSGT 204
Db 177 -----NALLNKGWVADSRFLMPVILRQCGEMFRGINSVLVDVGGH 216
QY 205 GITAKIICEAPFKLKCWLRLPNVVENLGSNNLTFVGGDMFKCIPKADAVLLKLVLHNV 264
Db 217 GGAATAAIAAFPHVKCSVLDPHVVAGAPSDGNVQFVAGNMFESIPPTAVFLKTLHDW 276
QY 265 NDNDCKMILENCKEKAISGESKTGVVITVINENKDERQVTELKLMVHMVACIINGKE 324
Db 277 GDCEVKILNCKQAIPPRDAGGKVIILDVVVGKQSNIKHQETQVMPDLYMA-VNGVE 335
QY 325 RKEEDWKLFEVAGFQSKISPFTGYLS-LIEIYP 358
Db 336 RDEQWKKIFAEAGFKDYKILPVIIGDVSIIIEVYP 370
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RESULT 3
US-10-361-460-7
; Sequence 7, Application US/10361460
; Publication No. US20030163839A1
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
; FILE REFERENCE: 0709
; CURRENT APPLICATION NUMBER: US/10/361,460
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/057,082
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Zea mays
US-10-361-460-7

Query Match 28.7%; Score 540.5; DB 12; Length 366;
Best Local Similarity 33.3%; Pred. No. 9.5e-47;
Matches 128; Conservative 70; Mismatches 125; Indels 61; Gaps 11;

QY 11 ASEIFQGOALLYKHLGLFIDSKLKMVVELDIPDIHSHSHGQPIITFSELVSILOVPTK 70
Db 8 SODLLEAHDELFLHCLCFKSLALAVACDLRIPDAIHGGG--ATLHQAIAEALHPSK 65
QY 71 TRQVOSLMRYLAHNGFFEIVRIHNEIA-----YALTAASELLVKSSE---LSLAPM 119
Db 66 LRALERLMRVLTVTGTF--TVQYSSVTVDASDCADVYVRLTAASRFLVSDDEAGTASLAPF 124
QY 120 VEYFL-----EPNCOG--ANNQLK-----WHEEDLTVEVSLGTGTFW 156
Db 125 ANLAHLFIATSPHAGICAMFRQCHDPSPYGLAFROTPTLWEHADNV----- 172
QY 157 DFINKDPAYNKSFNEMACDSQ-MLNLAFRDC-NWVFEGLSIVDVGSGTGITAKIICEA 214
Db 173 -----NALLNKGLLABSRFLMPVILRECGEVEFRGIDSLVDVGGHGAATAIAA 223
QY 215 PPKLKCMVLERPNVVENLGSNNLTFVGGDMFKCIPKADAVLLKLVLHNMNDCKMILE 274
Db 224 PPHVKCSVLDPHVVAGAPSDACVQFVAGNMFHSIPPTAVFFKTTLCWDGDDCEIKLK 283
QY 275 NCKEAIAGESKTGVVITVINENKDERQVTELKLMVHMVACIINGKERKEDWKL 334
Db 284 NCKQAISPRDEGGKVIIMDVVVGQSNMKRLETQVMPDLYMA-VNGVERDEQEWKMF 342
QY 335 MEAGFQSKISPFTGYLSLIEIYP 358
Db 343 IEAGFKDYKIRPVAGLMSVIEVYP 366

RESULT 4
US-10-361-460-4
; Sequence 4, Application US/10361460
; Publication No. US20030163839A1
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
; FILE REFERENCE: 0709
; CURRENT APPLICATION NUMBER: US/10/361,460
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/057,082
; NUMBER OF SEQ ID NOS: 85
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Zea mays
US-10-361-460-4

Query Match
Best Local Similarity 23.1%; Score 435; DB 12; Length 354;
Matches 123; Conservative 60; Mismatches 147; Indels 32; Gaps 12;

QY 12 SEIFQOALLYKHLGFDISKCLKMWVELDIPDIHSHSHGQPIITSELSVLQVPPTKT 71
Db 10 AELLOAQADLPHSHSYLLTSMALKCAVELHIPTAI--HNLGGSATLPDVAALSIPAACL 67
QY 72 RQVQSLMYLAHNGFPEIURIHDNTEAYALTAASSELLVKSSELSAPVVEYF---LEPN 127
Db 68 PFLGRVRLVTSGVF---ASSDDVQ-YRLNPLSWLLVGVSESDHTYQYFVLVTGSRH 123
QY 128 COGAWNLKRWVHEED-----LTVFVSLGTPFWDFFINK--DPAYNKSFNEMAC-DSQ 178
Db 124 YVEAGMSLADWFKXSEDEDRQLPSPFEALHGVPLVHSTKLLDSELDRVVEEGVAHDNL 183
QY 179 MNLAFRCNW-VFGLSIVDVGCGTG-ITAKIICEAPPKLCMWLERPNVVENLSGN 236
Db 184 AIGTVIREGADVFGSLSLTYCCGRQGNASAAIVKAPPDIKCTVLNLRVVEETT-TK 242
QY 237 NLTFVGGDMFKCIPKADAVLLKVLHNNNDNCKILENCKEAKISGESKTKGVVVIDTVI 296
Db 243 TIT-----IPPAQAWLKLVLHFWDSDDCVILELCRAIISRQEGKVIIIEILL 293
QY 297 NENKDERQVTELKLMVDHMACIINGKERKEEDNKKLFMEAGFQSYKISPTFGYLSLIEI 356
Db 294 GPYMG-P-VWYEAQLMDMLMVNTKRGQRGEDDWRHIETKAGFSYKVVVKIGARGVIEV 352
QY 357 YP 358
Db 353 YP 354

RESULT 5
US-09-947-027-6
; Sequence 6, Application US/09947027
; Patent No. US20020124281A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 365
; TYPE: PRT
; ORGANISM: aspen populus tremuloides
US-09-947-027-6

Query Match
Best Local Similarity 19.7%; Score 371.5; DB 10; Length 365;
Matches 97; Conservative 69; Mismatches 132; Indels 29; Gaps 8;

QY 34 LKMWVELDIPDIHSHSHGQPIITSELSVLQVPPTKR---QVQSLMRYLAHNGFF-- 87
Db 36 LKTAIELDLLEIMAKAGFGAFLSTSEIASHL---PTKNPDAPVMDRLIRLLASYSILTC 92
QY 88 -----EIVRIHDNIEAYALTAASSELLVKSSE-LSLAPMVVEYFLEPNCOGAWNLKRW 138
Db 93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPCLMNQDKVLMESWYLLXDA 146
QY 139 VHEEDLTVEVSLGTPFWDFFINKDPAYNKSFNEMACDSOMLNLAFRCNWNVFEGLSIV 198
Db 147 ILDGGIP-FNKAYGWTAFEHGTDPRFNKVFKNKMSDHSHTIMKKILETYGFGELTSLV 205
QY 199 DVGGGTGITAKIICEAPPKLCMWLERPNVVENLSGNLTFVGGDMFKCIPKADAVLLK 258
Db 206 DVGGGTGAVVNTIVSKYPSIKGINFDPHPVEDAPSYGVEHVGDMFVSPKADAVFMK 265
QY 259 LVLHNNNDNCKILENCKEAKISGESKTKGVVVIDTVINENKDERQVTELKLMVDHMA 317
Db 266 WICHDSDAHCLKFLKNCYDAL---PENGKVLVECILPVPADTSLATKGVVHVDVIMLA 322
QY 318 CIINGKERKEEDNKKLFMEAGFQSYKI 344
Db 323 HNPCKERTETEKEFEGLAGAGFGQFEV 349

RESULT 7
US-10-091-009-6
; Sequence 6, Application US/10091009
; Publication No. US20020138870A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/10/091,009
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 365
; TYPE: PRT
; ORGANISM: aspen populus tremuloides
US-10-091-009-6

Query Match
Best Local Similarity 19.7%; Score 371.5; DB 14; Length 365;
Matches 97; Conservative 69; Mismatches 132; Indels 29; Gaps 8;

QY 34 LKMWVELDIPDIHSHSHGQPIITSELSVLQVPPTKR---QVQSLMRYLAHNGFF-- 87
Db 36 LKTAIELDLLEIMAKAGFGAFLSTSEIASHL---PTKNPDAPVMDRLIRLLASYSILTC 92
QY 88 -----EIVRIHDNIEAYALTAASSELLVKSSE-LSLAPMVVEYFLEPNCOGAWNLKRW 138
Db 93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPCLMNQDKVLMESWYLLXDA 146
QY 139 VHEEDLTVEVSLGTPFWDFFINKDPAYNKSFNEMACDSOMLNLAFRCNWNVFEGLSIV 198
Db 147 ILDGGIP-FNKAYGWTAFEHGTDPRFNKVFKNKMSDHSHTIMKKILETYGFGELTSLV 205
QY 199 DVGGGTGITAKIICEAPPKLCMWLERPNVVENLSGNLTFVGGDMFKCIPKADAVLLK 258
Db 206 DVGGGTGAVVNTIVSKYPSIKGINFDPHPVEDAPSYGVEHVGDMFVSPKADAVFMK 265
QY 259 LVLHNNNDNCKILENCKEAKISGESKTKGVVVIDTVINENKDERQVTELKLMVDHMA 317
Db 266 WICHDSDAHCLKFLKNCYDAL---PENGKVLVECILPVPADTSLATKGVVHVDVIMLA 322
QY 318 CIINGKERKEEDNKKLFMEAGFQSYKI 344
Db 323 HNPCKERTETEKEFEGLAGAGFGQFEV 349
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Zea mays
US-10-361-460-4

Query Match
Best Local Similarity 23.1%; Score 435; DB 12; Length 354;
Matches 123; Conservative 60; Mismatches 147; Indels 32; Gaps 12;

QY 12 SEIFQOALLYKHLGFDISKCLKMWVELDIPDIHSHSHGQPIITSELSVLQVPPTKT 71
Db 10 AELLOAQADLPHSHSYLLTSMALKCAVELHIPTAI--HNLGGSATLPDVAALSIPAACL 67
QY 72 RQVQSLMYLAHNGFPEIURIHDNTEAYALTAASSELLVKSSELSAPVVEYF---LEPN 127
Db 68 PFLGRVRLVTSGVF---ASSDDVQ-YRLNPLSWLLVGVSESDHTYQYFVLVTGSRH 123
QY 128 COGAWNLKRWVHEED-----LTVFVSLGTPFWDFFINK--DPAYNKSFNEMAC-DSQ 178
Db 124 YVEAGMSLADWFKXSEDEDRQLPSPFEALHGVPLVHSTKLLDSELDRVVEEGVAHDNL 183
QY 179 MNLAFRCNW-VFGLSIVDVGCGTG-ITAKIICEAPPKLCMWLERPNVVENLSGN 236
Db 184 AIGTVIREGADVFGSLSLTYCCGRQGNASAAIVKAPPDIKCTVLNLRVVEETT-TK 242
QY 237 NLTFVGGDMFKCIPKADAVLLKVLHNNNDNCKILENCKEAKISGESKTKGVVVIDTVI 296
Db 243 TIT-----IPPAQAWLKLVLHFWDSDDCVILELCRAIISRQEGKVIIIEILL 293
QY 297 NENKDERQVTELKLMVDHMACIINGKERKEEDNKKLFMEAGFQSYKISPTFGYLSLIEI 356
Db 294 GPYMG-P-VWYEAQLMDMLMVNTKRGQRGEDDWRHIETKAGFSYKVVVKIGARGVIEV 352
QY 357 YP 358
Db 353 YP 354

RESULT 5
US-09-947-027-6
; Sequence 6, Application US/09947027
; Patent No. US20020124281A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 365
; TYPE: PRT
; ORGANISM: aspen populus tremuloides
US-09-947-027-6

Query Match
Best Local Similarity 19.7%; Score 371.5; DB 10; Length 365;
Matches 97; Conservative 69; Mismatches 132; Indels 29; Gaps 8;

QY 34 LKMWVELDIPDIHSHSHGQPIITSELSVLQVPPTKR---QVQSLMRYLAHNGFF-- 87
Db 36 LKTAIELDLLEIMAKAGFGAFLSTSEIASHL---PTKNPDAPVMDRLIRLLASYSILTC 92
QY 88 -----EIVRIHDNIEAYALTAASSELLVKSSE-LSLAPMVVEYFLEPNCOGAWNLKRW 138
Db 93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPCLMNQDKVLMESWYLLXDA 146
QY 139 VHEEDLTVEVSLGTPFWDFFINKDPAYNKSFNEMACDSOMLNLAFRCNWNVFEGLSIV 198
Db 147 ILDGGIP-FNKAYGWTAFEHGTDPRFNKVFKNKMSDHSHTIMKKILETYGFGELTSLV 205
QY 199 DVGGGTGITAKIICEAPPKLCMWLERPNVVENLSGNLTFVGGDMFKCIPKADAVLLK 258
Db 206 DVGGGTGAVVNTIVSKYPSIKGINFDPHPVEDAPSYGVEHVGDMFVSPKADAVFMK 265
QY 259 LVLHNNNDNCKILENCKEAKISGESKTKGVVVIDTVINENKDERQVTELKLMVDHMA 317
Db 266 WICHDSDAHCLKFLKNCYDAL---PENGKVLVECILPVPADTSLATKGVVHVDVIMLA 322
QY 318 CIINGKERKEEDNKKLFMEAGFQSYKI 344
Db 323 HNPCKERTETEKEFEGLAGAGFGQFEV 349

RESULT 7
US-10-091-009-6
; Sequence 6, Application US/10091009
; Publication No. US20020138870A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/10/091,009
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 365
; TYPE: PRT
; ORGANISM: aspen populus tremuloides
US-10-091-009-6

Query Match
Best Local Similarity 19.7%; Score 371.5; DB 14; Length 365;
Matches 97; Conservative 69; Mismatches 132; Indels 29; Gaps 8;

QY 34 LKMWVELDIPDIHSHSHGQPIITSELSVLQVPPTKR---QVQSLMRYLAHNGFF-- 87
Db 36 LKTAIELDLLEIMAKAGFGAFLSTSEIASHL---PTKNPDAPVMDRLIRLLASYSILTC 92
QY 88 -----EIVRIHDNIEAYALTAASSELLVKSSE-LSLAPMVVEYFLEPNCOGAWNLKRW 138
Db 93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPCLMNQDKVLMESWYLLXDA 146
QY 139 VHEEDLTVEVSLGTPFWDFFINKDPAYNKSFNEMACDSOMLNLAFRCNWNVFEGLSIV 198
Db 147 ILDGGIP-FNKAYGWTAFEHGTDPRFNKVFKNKMSDHSHTIMKKILETYGFGELTSLV 205
QY 199 DVGGGTGITAKIICEAPPKLCMWLERPNVVENLSGNLTFVGGDMFKCIPKADAVLLK 258
Db 206 DVGGGTGAVVNTIVSKYPSIKGINFDPHPVEDAPSYGVEHVGDMFVSPKADAVFMK 265
QY 259 LVLHNNNDNCKILENCKEAKISGESKTKGVVVIDTVINENKDERQVTELKLMVDHMA 317
Db 266 WICHDSDAHCLKFLKNCYDAL---PENGKVLVECILPVPADTSLATKGVVHVDVIMLA 322
QY 318 CIINGKERKEEDNKKLFMEAGFQSYKI 344
Db 323 HNPCKERTETEKEFEGLAGAGFGQFEV 349
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US-09-796-256A-6
; Sequence 6, Application US/09796256A
; Patent No. US2002007847A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Carraway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617/c-3532.0
; CURRENT FILING DATE: 2001-02-28
; PRIOR FILING DATE: 1996-12-16
; PRIOR FILING DATE: 1996-12-16
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Liquidambar styraciflua
US-09-796-256A-6

Query Match      18.6%; Score 350.5; DB 9; Length 368;
Best Local Similarity 29.0%; Pred. No. 3e-27;
Matches 100; Conservative 62; Mismatches 130; Indels 53; Gaps 11;

Qy 34 LKWWVELDIPDIHSHSHGQPTITSELVSL--QVPTKTRQVQSLMRYLHNGFFEIVR 89
Db 38 LKSAIELELVLEIMAXAGFGAHIISTDIASKL---PTKNPDAAVMLDRMLRLLA----- 87

Qy 90 VRHNDIEAYALTAASELLVKSSSEL-----SLAPMVEYFLEPNCQGA-----WNO---- 134
Db 88 -----SYSLTCSLTLPDKGRLYRGLAPVCK-FLTRNDGQVSTAALSLMNQDKYL 138

Qy 135 LKRWWHEEDLTVEFVSLGTFP-----WDFINKDPAYNKSFNEMACDSQMLMLAFRD 186
Db 139 MESWYH---LTEAVLEGGIPFNKAYGMTAFYHGTDPRTNVTFNNGMSNHSTITMKKILE 195

Qy 187 CNWVPEGLESIVDGGGTGITAIIICEAPFKLKMVLERNPVNENLGSNNLTFVGGDMF 246
Db 196 TYKFGEGISVVDGGGTGAHLNMIIAKYPMIKGINFDLPVHIEAPSYPGVHVGDMF 255

Qy 247 KCIPKADAVLLKLVLHNMNDCKMILENCKEAISSGSKTGKVVVIDTVINENKDERQVT 306
Db 256 VSVPKGDAIFMKWICHDSDEHCLFKKCYEAL---PTNGKVILAECLPVPADASLPT 312

Qy 307 ELKLLMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYKISPTGY 350
Db 313 KAVVHIDVIMLAHNPGGKERTKEPEALAKAGPFGPRVASCAY 357

RESULT 8
US-10-289-757-103
; Sequence 103, Application US/10289757
; Publication No. US20030180751A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Forster, Richard L
; APPLICANT: Gibson, John Bryan
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: No. US20030180751A1riss, Geoffrey
; APPLICANT: Glenn, Matthew
; APPLICANT: Saulsbury, Keith Martin
; APPLICANT: Hall, Claire
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use
; FILE REFERENCE: 11000.1061U
; CURRENT FILING DATE: 2002-11-07
; PRIOR FILING DATE: 2002-11-07
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-289-757-102

Query Match      17.6%; Score 331.5; DB 12; Length 360;
Best Local Similarity 28.0%; Pred. No. 2.6e-25;
Matches 94; Conservative 65; Mismatches 128; Indels 49; Gaps 11;

Qy 34 LKWWVELDIPDIHSHSHGQPTITSELVSL--QVPTKTRQVQSLMRYLHNGFFEIVR 91
Db 33 LKNAIEGLLEILVA-AGGKSLTPTTEVAAKLPASAANPEAPDMVDRMLRLLA----- 82

Qy 92 IHDNIEAYALTAASELLVKSSSEL-----LAPMVEYFLEPNCQGA-----WNO----LK 136
Db 83 -----SYNVVTVCLVEBCKDGRLSRSYGAAPVCK-FLTPNEDGYMAALALMNQDKVLM 135

Qy 137 RWHEEDLTV-----FEVSLGTFPWFNDINKDPAYNKSFNEMACDSQMLMLAFRD 191
Db 136 SWYLYKDAVLDGGIPFNKAYGMTAFYHGTDPRTNVTFNNGMSNHSTITMKKILEYHGF 195

Qy 192 EGLSIVDVGSGGTGITAIIICEAPFKLKMVLERNPVNENLGSNNLTFVGGDMFKCIPK 251
Db 196 EGLSIVDVGSGGTGATVAAIAAHYPTIKGVNFDLPVHIEAPQFPGVTHVGGDMFKFVPS 255

Qy 252 ADAYLLKLVLHNMNDCKMILENCKEAISSGSKTGKVVVIDTVI-----NENKDERQVTE 307
Db 256 GDAILMKWILLHDSQHCATLLKNCYDALPAH---GKVLVECLPVPNPEANPSSQGVFH 312

Qy 308 LKLLMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYK 343
Db 313 VDMITLAHNP---GGRERYEREFOALARGAGFTGVK 345

RESULT 9
US-10-289-757-102
; Sequence 102, Application US/10289757
; Publication No. US20030180751A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Forster, Richard L
; APPLICANT: Gibson, John Bryan
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: No. US20030180751A1riss, Geoffrey
; APPLICANT: Glenn, Matthew
; APPLICANT: Saulsbury, Keith Martin
; APPLICANT: Hall, Claire
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use
; FILE REFERENCE: 11000.1061U
; CURRENT FILING DATE: 2002-11-07
; PRIOR FILING DATE: 2002-11-07
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-289-757-102

Query Match      17.6%; Score 331.5; DB 12; Length 360;
Best Local Similarity 28.0%; Pred. No. 2.6e-25;
Matches 94; Conservative 65; Mismatches 128; Indels 49; Gaps 11;

Qy 34 LKWWVELDIPDIHSHSHGQPTITSELVSL--QVPTKTRQVQSLMRYLHNGFFEIVR 91
Db 33 LKNAIEGLLEILVA-AGGKSLTPTTEVAAKLPASAANPEAPDMVDRMLRLLA----- 82

Qy 92 IHDNIEAYALTAASELLVKSSSEL-----LAPMVEYFLEPNCQGA-----WNO----LK 136
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Db 83 -----SYNVVTCVVECKDCKLSRSYGAAPVCK-FLTPNEDGVSMALALMNQKVLME 135
Qy 137 RWVHEEDLTV-----FEVSLGTFPPWDFINKOPAYNKSNFNEAMACDSQMLNLAFRDCNVWF 191
Db 136 SWYLYKDAVLDDGGPPFNKAYGMSAFYHGTDPFRNVRNVEGKNHSHIITTKLLELYHGF 195
Qy 192 EGLSEIVDVGGGTGTAKIIIEAFPKLKMVLERPVVENLSSNNLTFVGGDMFKCIPK 251
Db 196 QGLGTLVDVGGVGATVAAIAAHYPAIKGVNFDLPHVISEAPQPPGVTHVGGDMFKYEPS 255
Qy 252 ADAVLLKLVHNNNDCKMILENCKEAIKSGESKTKGVVVIDTVINENKDERQ-----VTE 307
Db 256 GDAILMKWLHDSQHCATLLKNCYDALPAH---GKVLVECILPVNPEAKPSSQGVFH 312
Qy 308 LKLLMDVHMCIINGKERKEEDWKKLFMEAGFQSYK 343
Db 313 VDMIMLAHP---GGREYEREFELARGAGFTGVK 345

RESULT 10
US-10-289-757-182
; Sequence 182, Application US/10289757
; Publication No. US20030180751A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jerroen
; APPLICANT: Forster, Richard L
; APPLICANT: Gibson, John Bryan
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: No. US20030180751A1riss, Geoffrey
; APPLICANT: Glenn, Matthew
; APPLICANT: Saulsbury, Keith Martin
; APPLICANT: Hall, Claire
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use
; FILE REFERENCE: 11000.1061U
; CURRENT APPLICATION NUMBER: US/10/289,757
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/337,703
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-10-289-757-182

Query Match 17.6%; Score 331.5; DB 12; Length 360;
Best Local Similarity 28.0%; Pred. No. 2.6e-25;
Matches 94; Conservative 65; Mismatches 128; Indels 49; Gaps 11;

Qy 34 LKMWVLDIPDIHSHSHGQITSELSVIL--QVPPKTRQVOSLMRYLAHNGFFFEIVR 91
Db 33 LKNAIEGLLELIVA-AGGKSLTTEVAAKLPSAANPEAPDMVDRMLRLA-----82
Qy 92 IHDNIEAYALTAASSELLVKSELS-----LAPWVEYFLPNCQGA-----WNO-136
Db 83 -----SYNVVTCVVECKDCKLSRSYGAAPVCK-FLTPNEDGVSMALALMNQKVLME 135
Qy 137 RWVHEEDLTV-----FEVSLGTFPPWDFINKOPAYNKSNFNEAMACDSQMLNLAFRDCNVWF 191
Db 136 SWYLYKDAVLDDGGPPFNKAYGMSAFYHGTDPFRNVRNVEGKNHSHIITTKLLELYHGF 195
Qy 192 EGLSEIVDVGGGTGTAKIIIEAFPKLKMVLERPVVENLSSNNLTFVGGDMFKCIPK 251
Db 196 QGLGTLVDVGGVGATVAAIAAHYPAIKGVNFDLPHVISEAPQPPGVTHVGGDMFKYEPS 255
Qy 252 ADAVLLKLVHNNNDCKMILENCKEAIKSGESKTKGVVVIDTVINENKDERQ-----VTE 307
Db 256 GDAILMKWLHDSQHCATLLKNCYDALPAH---GKVLVECILPVNPEAKPSSQGVFH 312
Qy 308 LKLLMDVHMCIINGKERKEEDWKKLFMEAGFQSYK 343
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Db 313 VDMIMLAHP---GGREYEREFELARGAGFTGVK 345

RESULT 11
US-10-289-757-105
; Sequence 105, Application US/10289757
; Publication No. US20030180751A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jerroen
; APPLICANT: Forster, Richard L
; APPLICANT: Gibson, John Bryan
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: No. US20030180751A1riss, Geoffrey
; APPLICANT: Glenn, Matthew
; APPLICANT: Saulsbury, Keith Martin
; APPLICANT: Hall, Claire
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use
; FILE REFERENCE: 11000.1061U
; CURRENT APPLICATION NUMBER: US/10/289,757
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/337,703
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-289-757-105

Query Match 17.5%; Score 329.5; DB 12; Length 361;
Best Local Similarity 27.8%; Pred. No. 4.2e-25;
Matches 103; Conservative 70; Mismatches 137; Indels 61; Gaps 14;

Qy 8 GRKASEIFQG---QALLYKHLG--FIDSKLKMVELDIPDIHSHSHGQITSELSVLS 62
Db 2 GSTAAETASAADBEACLYALQSSSLPMTLTKTILGLLETLMA-AGKSLTPTVAA 60
Qy 63 ILQVP---PTKTRQVOSLMRYLAHNGFFFEIVRHDNTEAYALTAASELLVK-----SS 112
Db 61 KLPCAANKPEAPDMVDRMLRLA-----SYNLVSC---LVEEGTDGLSLR 102
Qy 113 ELSLAPMVVEYFLPNCQGA-----WNO---LKRWHEDLTV-----FEVSLGTFPW 156
Db 103 RYGAAPVCK-FLTPNEDGVSMALALMNQKVLMEVLYLKDAVLDDGGIPFNKAYGMSAF 161
Qy 157 DFINKDPAYNKSNFNEAMACDSQMLNLAFRDCNVWFEGLESIVDVGGGTGTAKIICEAFP 216
Db 162 EYHGTDLRFNRVFNKNNNSIITKLLQLYDGFQGLGLTLVDVGGVGATVAAITAHYP 221
Qy 217 KLCOMVLERPVVENLSSNNLTFVGGDMFKCIPKADAVLLKLVHNNNDCKMILENC 276
Db 222 TIKGINFDLPHVISEAPPPGVTHIGDMFKKVPVSGDAILMKWLHDSQHCATLLKNC 281
Qy 277 KEAISGSKTKGVVVIDTVINENKDERQ-----VTELKLLMDVHMCIINGKERKEEDWKK 332
Db 282 YDALPVH---GKVLVECILPVNPEAKPSSQGVFHVDMIMLAHP---GGREYEREYEA 335
Qy 333 LFMEAGFQSYK 343
Db 336 LARGAGFAGFK 346

RESULT 12
US-10-289-757-104
; Sequence 104, Application US/10289757
; Publication No. US20030180751A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jerroen
; APPLICANT: Forster, Richard L
; APPLICANT: Gibson, John Bryan
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Db 290 CVKVLKNCWEAL---PPTGKVVIVEEVTPEYPCITDDVSQTL 328

RESULT 15

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US-09-953-348-133
; Sequence 133, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqing
; APPLICANT: Vargolu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530U51
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 351
; TYPE: Prt
; ORGANISM: Streptomyces lavendulae
US-09-953-348-133

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```

Query Match      14.5%; Score 273.5; DB 12; Length 351;
Best Local Similarity 27.0%; Pred. No. 2.2e-19;
Matches 95; Conservative 68; Mismatches 140; Indels 49; Gaps 15;

QY      25  LLGFIDSKCLKMVMVELDIPDIHSHSGQITITSELVSIIVQPTTKRVQOSLMRYIAHN 84
Db      26  LQGANAKARAHVAVELGVPELLOB---GPRATATA---EATGAHEQTILRLRLLATV 78
QY      85  GFTEIVRIHDNIYAYALTAASELLVKSSELSLAPMVEYFLEPNCQAGWNLKRWVHEDL 144
Db      79  GVFDDELG-HDDL--FAQNALSAVLLPDPASPVATDARFQAAPHWRAWEQITHSVRTGEA 135
QY      145  TVFEV-----SLGTPFWDFINKDPAYKNFNEAMACDSQMLNLAFRDCNWV-----FEG 193
Db      136  SPFSTWPTAPRSGSSP-----TRDPKARELFNRAMG-----SVSLTEACQVAAAVDFSG 184
QY      194  LESIVDVGGGTGITAKTICEAFKLCMWLERBNVYEN-----LSG-----SNNLTFVGGDMF 246
Db      185  AATAVDIGGGRGSLMAAVLDAFPLGRITLLRPVPAEEARELUTGRGLADRCITLPGDFF 244
QY      247  KCIPK-ADAVLLKLVLHNMWNDNCKMILENCKEPAISGESKTGKVVITDTVINENKDERQV 305
Db      245  ETIPDGADVLYIKHVLHWDWDDVVIRLRIRIATAMKPDs---RLVYIDNLI-----DERPA 297
QY      306  TELKLLMDVHMACIINGKERKEBDWKLFMEAGFQSYKISPF-TGYLSLIEI 356
Db      298  AS-TLFDVLLLVVGAASESEFAALLBKSGIRVERSLPCGAGPVRIVEI 348

```

Search completed: November 10, 2003, 03:30:38
Job time : 77 secs

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OM protein - protein search, using sw model

Run on: November 10, 2003, 03:09:40 ; Search time 43 Seconds
(without alignments)
800.660 Million cell updates/sec

Title: US-09-868-547-4
Perfect score: 1886
Sequence: 1 MASSLNNGRKASEIFQGOAL.....FQSYKISPTGYLSLIEIYP 358

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:***
1: PIR1:***
2: PIR2:***
3: PIR3:***
4: PIR4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1295	68.7	352	2 T09254	isoflavone-7-O-met
2	1285	68.1	352	2 T05707	isoflavone-O-meth
3	1237.5	65.6	343	2 T09299	O-methyltransferas
4	867.5	46.0	360	2 T05786	6a-hydroxymaackia
5	652.5	34.6	390	2 S52015	catechol O-methyl
6	606	32.1	364	2 JQ2268	O-methyltransferas
7	529.5	28.1	382	2 T09600	catechol O-methyl
8	527	27.9	382	2 T04963	catechol O-methyl
9	485	25.7	325	2 T04962	catechol O-methyl
10	426	22.6	363	2 T01354	herbicide safener
11	390.5	20.7	364	2 S36403	catechol O-methyl
12	386.5	20.5	364	2 S36404	catechol O-methyl
13	384	20.4	372	2 T09617	O-diphenol-O-meth
14	383.5	20.3	359	2 T12259	isoliquiritigenin
15	379.5	20.1	365	2 T09673	O-diphenol-O-meth
16	371.5	19.7	365	2 S18568	caffeate O-methyl
17	362.5	19.2	364	2 T09780	lignin-bispecific
18	358.5	19.0	366	2 JQ2146	probable caffeate
19	351	18.6	365	2 S40344	catechol O-methyl
20	342	18.1	363	2 E96559	catechol O-methyl
21	327.5	17.4	364	2 T28612	hypothetical prote
22	326	17.3	376	2 T06189	catechol O-methyl
23	322.5	17.1	350	2 T12260	probable catechol
24	318.5	16.9	367	2 E96796	caffeoyl-CoA O-met
25	316.5	16.8	352	2 H86454	hypothetical prote
26	303	16.1	359	2 T46160	CDS protein F9L11
27	303	16.1	365	2 S22696	caffeic acid O-met
28	299.5	15.9	381	2 H96656	myo-inositol O-met
29	283.5	15.0	381	2 F96804	hypothetical prote

30	283.5	15.0	381	2 G96804	hypothetical prote
31	278.5	14.8	373	2 B83444	hypothetical prote
32	278.5	14.8	373	2 B83444	hypothetical prote
33	272.5	14.4	373	2 B83444	hypothetical prote
34	271.5	14.4	373	2 B83444	probable O-methyl
35	268	14.2	356	2 A47128	carinomycin 4-O-m
36	257	13.6	334	2 F83120	probable O-methyl
37	252	13.4	376	2 J01393	O-demethylpuromyci
38	245.5	13.0	205	2 E96653	hypothetical prote
39	240.5	12.8	341	2 J05855	polyketide synthas
40	202	10.7	494	2 S27696	tcMw protein - Str
41	200.5	10.6	339	2 F70932	hypothetical prote
42	194	10.3	345	2 A42106	acetylserotonin O-
43	192	10.2	346	2 S21265	acetylserotonin O-
44	176	9.3	373	2 I37463	acetylserotonin O-
45	170.5	9.0	379	2 T50751	hydroxyneurosporen

ALIGNMENTS

RESULT 1

T09254
isoflavone-7-O-methyltransferase (EC 2.1.1.1.-) 9 - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09254
R:He, X.Z.; Reddy, J.T.; Dixon, R.A.
Plant Mol. Biol. 36, 43-54, 1998
A:Title: Stress responses in alfalfa (Medicago sativa L.) XXII. cDNA cloning and chara
A:Reference number: Z16628; MUID:98145455; PMID:9484461
A:Accession: T09254
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <HEX>
A:Cross-references: EMBL:AF000976; NID:g2580583; PIDN:AAC4927.1; PID:g9580584
C:Genetics:
A:Note: 7-10MT(9)
C:Function:
A:Description: catalyzes the O-methylation of A-ring hydroxyl group(s) of isoflavones;
A:Note: elicitor-inducible
C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase

Query Match	88.7%	Score	1295	DB	2	Length	352
Best Local Similarity	68.2%	Pred. No.	2.7e-96				
Matches	244	Conservative	55	Mismatches	53	Indels	6
						Gaps	4
QY	1	MASSLNNGRKASEIFQGOALLYKHLGFDGKCLKMWVLEDPDIHSHSGQITFSEL	60				
DB	1	MASSI-NGRKSEIFKQALLYKHYYAFIDMSLKWAVGMNIPNII--HNHGKPLSLNL	57				
QY	61	VSILQVPTKTRQVQSLMRYLAHNGPFPIVRIHNIAYALTAASELVKSELSLAEMV	120				
DB	58	VSILQVPSKICGNVRLMRYLAHNGFPIITKEE--ESYALTVASELLVRGSDCLAPWV	115				
QY	121	EYFLEPNCQGANOLKRWHEEDLTVEVSLGTFFPWPINKDPAYKSNFEMACDSQML	180				
DB	116	ECVLDPTLGSYHELKWKWYEEDLTFLGVTLSGFWDFLDKNPEYNTSFNDAMASDKLI	175				
QY	181	NLAFRDCNWPEGLSEIVDVGGGTGITAKICEAPPKLKMVLERNVVENLGSNNLTF	240				
DB	176	NLAURDCDFVDGLSEIVDVGGGTGITAKICEFTFKKLCIVFRPQVENLGSNNLTY	235				
QY	241	VGGDMFKCIPKADAVLLKLVLHNWNDCKMLNCKEAKISGESKTKGVVVIDVINEK	300				
DB	236	VGGDMFTSIPNADAVLLKYLHNWTDCLRLKCKEAVINDGKRGKVTIDVINEKK	295				
QY	301	DERQVTELKLMVDVHMACINGEKKEEDWKLPMEAGPQSYKISPTGYLSLIEIYP	358				
DB	296	DENQVTQIKLMDVNNMAC-LNGKERNNEEWKLPFEAGFQHYKISPLTGFLSLIEIYP	352				

QY 1 MASSLN-----NGRKAS-----EIFOQALLVKKLLGTFIDSKCLKMWVVELDIPDI 46
Db 1 MDSNGLAKSNGCEISRDGFFSEBEBELQQAEMKCTFAFAESLAVKCVLLGIPDMI 60
QY 47 HSHSHGQPIITFSELVSILOVPPKTRQVQSL---MRYLAHNGFF---EIVRIHDNIEA-Y 99
Db 61 AREGSRATLSGLSIVAKL---PTSPDAACLFIMRFLVAKGIFRASKAREGGAPETRY 117
QY 100 ALTAASSELLVKSSELSLAPMVEYFLEPNCQGANQLKRWVHEEDLTAVFEVSLGTPPWFPI 159
Db 118 GLTPASKWLKGRSLNAPLWQNDLTLAPHHNFECVLEGGV-AFQKANGAEIWSYA 176
QY 160 NKDPAYNKSNEAMACDSQMLNLAFRDNCWVFGLESIVDVGGTGITAKICEAPPKUK 219
Db 177 SDHPDFNNLFNNAACMACNVMKGIISLYQGFHSLNSLVDVGGTGITAEVIRAYPFIT 236
QY 220 CMVLERPNVVENLSSNNLTFVGGDMFKCIPKADAVLLKLVLNWNNDCMKILENCKEA 279
Db 237 GINYDLPHVVATASSLSGVHVGDMFETVPTGDAFMKWMHMDNDEDCIKLKCRKA 296
QY 280 ISGSKTKGVVIVDTVIN-----ENKDERQV-----TELKLLMDVHMVHACIINGKERKE 327
Db 297 I---PDTGKVIIVDVLWDAGDQNTDKKKAVIDPIVGTVPFLVMVMAHSS---GGRERSE 350
QY 328 EDWKKLFMEAGFQSKISPTGYLSLIEIYP 358
Db 351 KEWKRIILEGGFSRYNIIEIPALQSIVIEAPP 381

RESULT 8
T04963
catechol O-methyltransferase homolog T12J5.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
C:Accession: T04963
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, February 1999
A:Reference number: 215392
A:Accession: T04963
A:Molecule type: DNA
A:Residues: 1-382 <BEV>
A:Cross-references: EMBL:AL035522
A:Experimental source: cultivar Columbia; BAC clone T12J5
C:Genetics:
A:Map position: 4
A:Introns: 275/3
A:Note: T12J5.30
C:Superfamily: O-methyltransferase

Query Match 27.9%; Score 527; DB 2; Length 382;
Best Local Similarity 34.1%; Pred. No. 1.4e-34;
Matches 126; Conservative 70; Mismatches 151; Indels 22; Gaps 10;
QY 6 NNGRKA-SEIFQGOALLVKKLLGTFIDSKCLKMWVVELDIPDIHSHSGQPIITFSELVSI 64
Db 17 DNKKVLDDEAKASDIWKYVFGFADIAAKCAIDLKIPAEIENHPSSQPVTLAEUSSAV 76
QY 65 QVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNI-BAYALTAASE--LLVKSSELSLAPMVE 121
Db 77 SASPSHLRRI---MFLVHQGIKPEIPTKGLATGYNTPLSRRLMITRRDGKSLAPFVL 133
QY 122 YFLEPNCQGANQLKRW-----VHEEDLTVEVSLGTPPWFIDPKDYNKSNFNEAMACDS 177
Db 134 FETTEMLAPLRLSSVSVFNGSTPPPPFPAVHGKVMSPFAQDNFLSDMINEAMACDA 193
QY 178 -QMLNLAFRDNCWVFGLESIVDVGGTGITAKICEAPPKLCMWLERPNVVENLSSGN 236
Db 194 RRVPRVAGACHGLDGVTTWVDVGGGTGWTGMLVKEFPWIKGFNFDLPHVIEVAVELD 253
QY 237 NLTFVGGDMFKCIPKADAVLLKLVLNWNNDCMKILENCKEAISGESKTKGVVIVDTVI 296
Db 254 GVENVEGDMFDSIPACDAIFIKWHLWDGDKDCIKLKNCKEAV--PPNIGKVLIVESVI 311

QY 297 NENK-----DER--QVTELKLLMD-VHMACTIINGKERKEEDWKKLFMEAGFQSKISPT 348
Db 312 GENKKTWIVDERDEKLEHVRMLMDVMMAHTSTGKERTLKEWDFVLKEAGFAFYEVREDID 371
QY 349 GYLSLIEIY 357
Db 372 DVQSLIIAY 380
RESULT 9
T04962
catechol O-methyltransferase homolog T12J5.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999
C:Accession: T04962
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: 215392
A:Accession: T04962
A:Molecule type: DNA
A:Residues: 1-325 <BEV>
A:Cross-references: EMBL:AL035522
A:Experimental source: cultivar Columbia; BAC clone T12J5
C:Genetics:
A:Map position: 4
A:Introns: 109/1; 218/3
A:Note: T12J5.20
C:Superfamily: O-methyltransferase

Query Match 25.7%; Score 485; DB 2; Length 325;
Best Local Similarity 32.3%; Pred. No. 2.6e-31;
Matches 113; Conservative 64; Mismatches 115; Indels 58; Gaps 8;
QY 21 LYKLLGIDSKCLKMWVVELDIPDIHSHSGQPIITFSELVSILOVPPKTRQVQSLMRY 80
Db 19 IWRVYVFGFADIAAKCAIDLKIPAEIENHPSSQPVTLSELSSAVSASPSSLRRI---MRF 75
QY 81 LAHNGFPEIVRIHDNI-BAYALTAASELLVKSSELSLAPMVEYFLEPNCQGANQLKRW 139
Db 76 LVHQGLFKEVTKDGLATGYNTPLSRRLMITK-----L 109
QY 140 HEEDLTVEVSLGTPPWFIDPKDYNKSNFNEAMACDS-QMLNLAFRDNCWVFGLESIV 198
Db 110 HGKOL-----WAPAQDNLCHSOLINEAMACDARRVVRVAGACQGLFDGVATV 158
QY 199 DVGGGTGITAKICEAPPKLCMWLERPNVVENLSSGNLTFVGGDMFKCIPKADAVLLK 258
Db 159 DVGGGTGTMGLIVKEFPWIKGFNFDLPHVIEVAVELDGVENVEGDMFDSIPASDAVIK 218
QY 259 LVLNWNNDCMKILENCKEAISGESKTKGVVIVDTVINENK-----ERQVTE 307
Db 219 WYLDWDGDKDCIKLKNCKEAVL--PNIGKVLIVECVIGKKNTWIAEERDDKLEHVRQL 276
QY 308 LKLLMDVHMACTIINGKERKEEDWKKLFMEAGFQSKISPTGYLSLIEIY 357
Db 277 LDMVMVMVHTS---TGKERTLKEWDFVLTEAGFAFYEVREDIDVQSLIIAY 323
RESULT 10
T01354
herbicide safener binding protein 1 - maize
C:Species: Zea mays (maize)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Oct-1999
C:Accession: T01354
R:Scott-Craig, J.S.; Casida, J.E.; Poduje, L.; Walton, J.D.
Plant Physiol. 116, 1083-1089, 1998
A:Title: Herbicide safener-binding protein of maize. Purification, cloning, and expres
A:Reference number: Z14299; MUID:98169422; PMID:9501141
A:Accession: T01354
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-363 <SCO>

```

Db      206 DVGGGTGATVNMIVSYKPSKINGINFLPHVIGDAPTYGVVHVHVGDMFASVPKADAIFMK 265
Qy      259 LVLHNWVNDNDCKMILENCKEAKESGSKTGKVVVIDVIVNENKDERQVTELKLLMDVHM-A 317
Db      266 WICHDSWDEHCLFKLNCVYEALPA---NGKVIIAECILPEAPDTSLATKNTVHVDIVMLA 322
Qy      318 CIINGKERKEEDWKLFMEAGFQSYKISPTGYLSLIEI 356
Db      323 HNPGGKERTKEPEALAKAG-----FTGPARLVAL 353

RESULT 12
S36404
catechol O-methyltransferase (EC 2.1.1.6) - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C:Accession: S36404
R:Legrand, M.
submitted to the EMBL Data Library, August 1993
A:Reference number: S36403
A:Accession: S36404
A:Molecule type: mRNA
A:Residues: 1-364 <LEG>
A:Cross-references: EMBL:X74453; NID:g396590; PID:g396591
C:Superfamily: O-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 20.5%; Score 386.5; DB 2; Length 364;
Best Local Similarity 30.1%; Pred. No. 2.4e-23;
Matches 102; Conservative 64; Mismatches 136; Indels 37; Gaps 8;

Qy      34 LKMVBLDIPDIHSHSGQPTIFSLVSIL-----QVPPTKTRQVQSLMRYLAHNGFPE 88
Db      36 LKSALELDLLEMAKAGCAAISPELAQLSTQNEAPVILDRMLRLATYSVLNCTLR 95
Qy      89 IVRIHNDIAYALTAASELLVKSSE-LSLAPWVEVLEFNCQAGNQ----LKRWVHEED 143
Db      96 TLSGDSVERLYSLAPVCKFLTKNADGVSAPLL-----LNNQDKVLMESWYHLKD 145
Qy      144 LTV-----FEVSLGTFFWPFINKDPAYNKSFEAMACDSOMLNLAFRDCNWNVFEGLSTV 198
Db      146 AVLDDGIGPNKAYGMTAFYHGTDFPNKVFNRGSHDSHSTNMKKILEDYKGFEGLSNV 205
Qy      199 DVGGGTGITAKICEAPFKLKCWLERPWNVENLSGSNNLTFVGGDMFKCIPKADAVLLK 258
Db      206 DVGGGTGATVNMIVSKHPSKINGINFLPHVIGDAPYGVVHVHVGDMFASVPKADAIFMK 265
Qy      259 LVLHNWVNDNDCKMILENCKEAKESGSKTGKVVVIDVIVNENKDERQVTELKLLMDVHM-A 317
Db      266 WICHDSWDEHCLFKLNCVYEALPA---NGKVIIAECILPEAPDTSLATKNTVHVDIVMLA 322
Qy      318 CIINGKERKEEDWKLFMEAGFQSYKISPTGYLSLIEI 356
Db      323 HNPGGKERTKEPEALAKAG-----FTGPARLVAL 353

RESULT 13
T09617
isoliquiritigenin 2'-O-methyltransferase - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09617
R:Maxwell, C.A.; Harrison, M.J.; Dixon, R.A.
Plant J. 4, 971-981, 1993
A:title: Molecular characterization and expression of alfalfa isoliquiritigenin 2'-O-
ion genes.
A:Reference number: Z16778; MUID:94108491; PMID:8281189
A:Accession: T09617
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-372 <MAX>
A:Cross-references: EMBL:L10211; NID:g289126; PIDN:AAB48059.1; PID:g1843462

```

A;Experimental source: subspecies sativa; cultivar Apollo
C;Function:

A;Description: methylates the 2'-hydroxyl of isoliquiritigenin (2',4',4'-trihydroxychalcone)
A;Note: 4,4'-dihydroxy-2-methoxychalcone is the most potent of the nod-gene-inducing flavonoids
C;Superfamily: O-methyltransferase
C;Keywords: methyltransferase

```
Query Match      20.4%; Score 384; DB 2; Length 372;
Best Local Similarity 28.5%; Pred. No. 4e-23;
Matches 103; Conservative 77; Mismatches 137; Indels 44; Gaps 12;

QY 30 DSKLKWV-----ELDIPDII-HSHSHGQPIITFSELVSILOVPPTKR- 72
Db 22 DSACLSAMVLTNLVYPAVLNAADLNLPELIATKATPPGAFMSPSEIASKL---PASTQH 78
QY 73 -----QVQSLMRYLAHNGPFEIVRIHDNIE-----AYALTAASELLV-KSSELSLAPMV 120
Db 79 SDLPNLRDRLRLA--SYSLVTSRTTIDGGGAERYGLSVGKYLVPDESRYLASFT 136
QY 121 EYFLEPNCQAGANQKLEWVHEEDLTVFVSLGTPTFMDPINKDPAYNKSFEAM--ACDSQ 178
Db 137 TFLCYPALLQVWVNFKAUVDEIDLPFNHVGTVKTFEPMGDKKMGQIFNKSVDVCATE 196
QY 179 MNLAFRCQWVPEGLSIVDVGGGTGITAIIICEAPPKLKMVLRPNVVENLGSNNL 238
Db 197 MKRML--EIVTGFEGISTLVGVGGSGRNLELIISKVPLIKGINFDLPQVIENAPPLSGI 254
QY 239 TFVGGDMFKICPKADAVLLKLVHNNDNDCKMLNCKEKAISGESKTKGVVVIDTVINE 298
Db 255 EHVGGDMFASVPGDAMILKAVCHNWSDEKICBFLSNCHKAL---SPNGKVIIVEFILPE 311
QY 299 NKDERQVTELKLMVDHMAICIIINGKERKEEDMKLFMEAGFQSYKIS--PFTGYLSLIEI 356
Db 312 EPNTSESKLVSLDNLMEITVGRERTERQYKELSKLSGFSKFOVACRAFNS-LGWMEF 370
QY 357 Y 357
Db 371 Y 371
```

RESULT 14

T12259
O-diphenol-O-methyltransferase (EC 2.1.1.-) - pepper
C;Species: Capsicum annuum (pepper)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C;Accession: T12259
R;Lee, B.; Choi, D.; Lee, K.W.
J. Plant Biol. 41, 9-14, 1998.
A;Title: Isolation and characterization of o-diphenol-O-methyltransferase cDNA Clone in
A;Reference number: Z17476
A;Accession: T12259
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-359 <EE>
A;Cross-references: EMBL:U83789; NID:g1791351; PID:g1791352
A;Experimental source: very young green fruit
C;Superfamily: O-methyltransferase
C;Keywords: methyltransferase

```
Query Match      20.3%; Score 383.5; DB 2; Length 359;
Best Local Similarity 31.3%; Pred. No. 4.1e-23;
Matches 103; Conservative 60; Mismatches 131; Indels 35; Gaps 8;

QY 34 LKMWVELDIPDIIHSHSHGQPIITFSELVSILOVPPTKT-----RQVQSLMRYLAHNG 85
Db 32 LKSALELDLLEIIMAKAGPGAQISPSLEAQL---PTKNPEAPVMDRLMRLLATYSLVLC 88
QY 86 FFEIVRIHNDIAYALTAASELLVKSE--LSLAPMVVEYFLEPNCQAGANQ---LKRWWH 140
Db 89 TLTLPDGRVERLYSLAPVCKLLTKQADGVSVAPLL-----LNNQDKVLMESVWH 138
QY 141 EEDLTV-----FEVSLGTPTFMDPINKDPAYNKSFEAMACDSQMLNLAFRDCQWVFEGL 195
```

```
Db 139 LTVDAVLDGGVFFNKAYGMTAFYHGTDPFRPNKVNRMGSDHSTMTWKKILEDKYGPGLN 198
QY 196 SIIVDVGGGTGITAIIICEAPPKLKMVLRPNVVENLGSNNLTFYGGDMFKICPKADAV 255
Db 199 SIIVDVGGGTGATVNMIVSKYPSIKGINFDLSHVIDEAPYPGVHVGRDMFVSPKADAI 258
QY 256 LKLVHNNNDNDCKMLNCKEKAISGESKTKGVVVIDTVINENKDERQVTELKLMVDVH 315
Db 259 FMKWI CHDWSDEHCLKFLKNCYEALPA---NGKVLVAECILPETPTDTSATKNAVHVDIV 315
QY 316 M-ACIINGKERKEEDMKLFMEAGFQSYK 343
Db 316 M-LAHNPGGKERTKEFEALAKAGAGTGFGR 344
```

RESULT 15

T09673
caffeate O-methyltransferase (EC 2.1.1.68) - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09673
R;Gowri, G.; Bugos, R.C.; Campbell, W.H.; Maxwell, C.A.; Dixon, R.A.
Plant Physiol. 97, 7-14, 1991.
A;Title: Molecular cloning and expression of alfalfa S-adenosyl-L-methionine: caffeic
A;Reference number: Z16815
A;Accession: T09673
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <GOW>
A;Cross-references: EMBL:M63853; NID:g166419; PID:g166420
A;Experimental source: subspecies sativa, cultivar Apollo
C;Function: lignin biosynthesis
A;Pathway: lignin biosynthesis
C;Superfamily: O-methyltransferase
C;Keywords: methyltransferase; S-adenosylmethionine

```
Query Match      20.1%; Score 379.5; DB 2; Length 365;
Best Local Similarity 31.4%; Pred. No. 8.9e-23;
Matches 106; Conservative 63; Mismatches 134; Indels 35; Gaps 10;
```

```
QY 34 LKMWVELDIPDIIHSHSHGQPIITFSELVSILOVPPTKTQVQSLMRYLAHNGFFEI---- 89
Db 36 LKSALELDLLEIIMAKAGPGAQISPIEIAS--OLPTNPDAFVMDRLMRLLATCYILTCS 93
QY 90 VRIHNISA---YALTAASELLVKSE--LSLAPMVVEYFLEPNCQAGANQ---LKRWWHE 141
Db 94 VRTQODGKVQRLYGLATVAKYLVKNEDGVVISAL-----LNNQDKVLMESVYHL 143
QY 142 EEDLTV-----FEVSLGTPTFMDPINKDPAYNKSFEAMACDSQMLNLAFRDCQWVFEGLS 196
Db 144 KDAVLDGGIPPNKAYGMTAFYHGTDPFRPNKVNRMGSDHSTMTWKKILETYTGFGLKS 203
QY 197 IVDVGGGTGITAIIICEAPPKLKMVLRPNVVENLGSNNLTFYGGDMFKICPKADAVL 256
Db 204 LVDVGGGTGAVINTIVSKYPTIKGINFDLPVIEDAPYPGVHVGRDMFVSPKADAVF 263
QY 257 LKLVHNNNDNDCKMLNCKEKAISGESKTKGVVVIDTVINENKDERQVTELKLMVDVH 316
Db 264 MKWICHDWSDEHCLKFLKNCYEAL---PDNGKVIVAECILPVAPDSSLATKGWVHIDVIM 320
QY 317 -ACIINGKERKEEDMKLFMEAGFQSYKI--SPFTGYL 351
Db 321 LAHNPGGKERTKEFEALAKAGAGTGFGR 358
```

Search completed: November 10, 2003, 03:22:07
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2003, 01:53:20 ; Search time 23 Seconds
(without alignments)
731.981 Million cell updates/sec

Title: US-09-868-547-4

Perfect score: 1886

Sequence: 1 MASSLNGKASEIFOGQAL.....FQYKISPTGYLSLFIETYP 358

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	636.5	33.7	347	1 60MT COPJA	Q9le16 Coptis japo
2	606	32.1	364	1 ZRPA MAIZE	P47917 zea mays (m
3	587.5	31.2	350	1 40MT COPJA	Q9le15 Coptis japo
4	390.5	20.7	350	1 40MT COPJA	Q81187 coffee cane
5	390.5	20.7	363	1 0MT1 APATH	Q9fk25 arabidopsis
6	383.5	20.3	359	1 0MT1 CAPAN	Q9fgv8 capsicum an
7	383.5	20.3	363	1 0MT1 CATRO	Q8w013 catharanthu
8	380	20.1	343	1 0MT1 CHRAE	P59049 chrysosplen
9	379.5	20.1	365	1 0MT1 MEDSA	P28002 medicago sa
10	379	20.1	343	1 0MT2 CHRAE	Q42853 chrysosplen
11	375.5	19.9	359	1 0MT1 CAPCH	O81646 capsicum ch
12	371.5	19.7	361	1 0MT1 OCIBA	Q9xgw0 ocimum basi
13	371.5	19.7	365	1 0MT1 POPTM	Q00763 populus tre
14	368.5	19.5	365	1 0MT1 POPKI	Q43046 populus kit
15	367.5	19.5	365	1 0MT1 PRUDU	Q43609 prunus dulc
16	366.5	19.4	364	1 0MT3 POPKI	Q43047 populus kit
17	363.5	19.3	361	1 0MT2 OCIBA	Q9xgv9 ocimum basi
18	362.5	19.2	364	1 0MT2 POPTM	Q41086 populus tre
19	358.5	19.0	366	1 0MT1 EUCGU	P46484 eucalyptus
20	356.5	18.9	365	1 0MT1 BOSCH	Q8gn25 rosa chinen
21	356	18.9	370	1 0MT1 CLABR	Q23760 clarkia bre
22	345	18.3	354	1 0MT1 ZINEL	Q43239 zinnia eleg
23	339.5	18.0	362	1 0MT1 SACOF	O82054 saccharum o
24	334.5	17.7	313	1 0MT1 EUCGL	Q39522 eucalyptus
25	332.5	17.6	381	1 SMT COPJA	Q39522 Coptis japo
26	327.5	17.4	364	1 0MT1 MAIZE	Q06509 zea mays (m
27	303	16.1	365	1 0MT1 WESCR	P45986 mesembryant
28	268	14.2	355	1 0MT1 STRPE	Q06528 streptomyc
29	252	13.4	376	1 0MT1 STRLP	P42712 streptomyc
30	202	10.7	494	1 TCNM STRGA	P16559 streptomyc
31	194	10.3	345	1 HIOM BOVIN	P10950 bos taurus
32	194	10.3	345	1 HIOM HUMAN	P46597 homo sapien
33	192	10.2	346	1 HIOM_CHICK	Q92056 gallus gall

RESULT 1

ID	60MT COPJA	STANDARD;	PRT;	347 AA.
AC	Q9le16;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	(R,S)-norcoclaurine 6-O-methyltransferase (EC 2.1.1.128) (S-adenosyl-L-methionine:norcoclaurine 6-O-methyltransferase) (6-OMT).			
DE	L-methionine:norcoclaurine 6-O-methyltransferase (EC 2.1.1.128) (S-adenosyl-L-methionine:norcoclaurine 6-O-methyltransferase) (6-OMT).			
OS	Coptis japonica (Japanese goldthread)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;			
OC	Ranunculaceae; Coptis.			
OX	NCBI_TaxID:3442;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20390108; PubMed-10811648;			
RA	Morishige T., Tsujita T., Yamada Y., Sato F.;			
RT	"Molecular characterization of the S-adenosyl-L-methionine:			
RT	3'-hydroxy-N-methylcoclaurine 4'O-methyltransferase involved in			
RT	isoquinoline alkaloid biosynthesis in Coptis japonica.";			
RL	J. Biol. Chem. 275:23398-23405(2000).			
RN	[2]			
RP	SEQUENCE OF 88-103, AND CHARACTERIZATION.			
RX	MEDLINE-95010097; PubMed-7925429;			
RA	Sato F., Tsujita T., Katagiri Y., Yoshida S., Yamada Y.;			
RT	"Purification and characterization of S-adenosyl-L-methionine:			
RT	norcoclaurine 6-O-methyltransferase from cultured Coptis japonica			
RT	cells.";			
RL	Eur. J. Biochem. 225:125-131(1994).			
CC	!- FUNCTION: CATALYZES THE TRANSFER OF THE S-METHYL GROUP OF S-			
CC	ADENOSYL-L-METHIONINE (ADOMET) TO THE 6-HYDROXYL GROUP OF			
CC	NORCOCCLAURINE TO FORM COCLAURINE.			
CC	!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + (R,S)-norcoclaurine			
CC	= S-adenosyl-L-homocysteine + (R,S)-coclaurine.			
CC	!- PATHWAY: CARRIES OUT A STEP IN THE CONVERSION OF 3'-HYDROXY-N-			
CC	METHYLCOCCLAURINE TO RETICULINE, AN IMPORTANT INTERMEDIATE IN			
CC	SYNTHESIZING ISOQUINOLINE ALKALOIDS.			
CC	!- SUBUNIT: Homodimer.			
CC	!- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; D29811; BAB08004.1; -			
DR	InterPro; IPR001601; Methyltransf.			
DR	InterPro; IPR001077; O-Metransf2.			
DR	Pfam; PF00691; Methyltransf_2; 1.			
KW	Transferase; Methyltransferase.			
SQ	SEQUENCE 347 AA; 38700 MW; 2BC34B3PBE67167C CRC64;			

O95671 homo sapien
P55790 aspergillus
Q12120 aspergillus
P54906 rhodobacter
P17061 rhodobacter
P39896 streptomyc
Q19020 caenorhabdi
P39073 saccharomyc
P35729 saccharomyc
P29220 homo sapien
O33768 sulfolobus
Q931e1 staphylococ

ALIGNMENTS

Query Match 33.7%; Score 636.5; DB 1; Length 347;
Best local Similarity 38.9%; Pred. No. 5.2e-44;
Matches 133; Conservative 70; Mismatches 132; Indels 7; Gaps 5;

QY 18 QALLVKKLLGLGIDSKCLKWVVELDIPDIHHSHSGQPITFFSELVSILQVPPTKTROVSL 77
DB :
Db 11 QAKLWNFIYGAEBSLVLCVAVOLDLANI--HNGTSMTLSELSRLPSQPVNEDALRV 68
:
QY 78 MRYLAHNAGFPFIVRIHDNIIEAYALTAAEELLVKSSLSLAPWEVFLEPNCGAANNOLKR 137
DB :
Db 69 MRYLVHMKLFTKASIDGELR-YGLAPPKYLKVGDCKMVGSIILAIDTKPFMAFWHYLDK 127
:
QY 138 WHHEEDITVFVSVISGTPPWFINDKPAYNKSPFNAMACDSQMLNAP-RDCNWVFEGLS 196
DB :
Db 128 GLSGESGTAFKALGTINIGYMAEPKNQLFNEAMANDSLIMSALKKECGNIFNGITT 187
:
QY 197 IVDVGGGTGITAKIICBAFFPKLKWLBRPNVENLGSNNLTFTVGGDMFKCIPKADAVL 256
DB :
Db 188 LVDVGGGTGTAVRNIAFAFHIKTVLDPLPHVIADSPGYSEVHCVAGDMFPKIPRADAIM 24
:
QY 257 LKVLHNNDNCMKLIENCKEA-SGESKTKGVVVDTVINENKDEROVTLEKLIMDVHM 316
DB :
Db 248 MKCILHDWDDECTEILKRCEAV-PVKGKGIIVDIVLN-V-QSEHPYTKWRILTLDLM 304
:
QY 317 ACIINGKERKEEDMKLFMEAGFSQYSKIPTFGVLSLIIETP 358
DB :
305 MLNTGGKERTEEEWKLIHDAGYKGHKITQITAVQSVEIAYP 346

RESULT 2

ZRP4_MAIZE STANDARD; PRT; 364 AA.

ID ZRP4_MAIZE

AC P47917;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE O-methyltransferase ZRP4 [EC 2.1.1.-] (OMT).

GN ZRP4

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=CV_KNH31; TISSUE=Root;
RX MEDLINE=94105316; PubMed=8278520;
RA Held B.M., Wang H., John I., Wurtele E.S., Colbert J.T.;
RT "An mRNA putatively coding for an O-methyltransferase accumulates
RT preferentially in maize roots and is located predominantly in the
RT region of the endodermis";
RL Plant Physiol. 102:1001-1008(1993).
CC -!- FUNCTION: MAY BE INVOLVED IN THE O-METHYLATION OF SUBERIN *.
CC -!- PHENYLPROPANOID PRECURSORS.
CC -!- TISSUE SPECIFICITY: ACCUMULATES PREFERENTIALLY IN THE ROOTS AND IS
CC LOCATED PREDOMINANTLY IN THE REGION OF THE ENDODERMIS, LOW LEVELS
CC ARE SEEN IN THE LEAVES, STEMS, AND OTHER SHOOT ORGANS.
CC -!- SIMILARITY: TO OTHER OMTs REQUIRING S-ADENOSYL-L-METHIONINE AS
CC SUBSTRATE.

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CC or send an email to license@sb-sib.ch).

DR EMBL: L14063; AAA18532.1; --
DR PIR: JQ2268; JQ2268.
DR Maiz6DB; 63528; --
DR InterPro: IPR001601; Methyltransf.
DR InterPro: IPR001077; O_Metransf2.

RT
RL
Biochim. Biophys. Acta 1353:199-202(1997).
[2]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:203-216(1998).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE OF 285-363 FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Green siliques;
RA Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
FUNCTION, AND CHARACTERIZATION.
RX MEDLINE=20166962; PubMed=10700397;
RT Muzac I., Wang J., Anzellotti D., Zhang H., Ibrahim R.K.;
RT "Functional expression of an Arabidopsis cDNA clone encoding a
RT flavonol 3'-O-methyltransferase and characterization of the gene
RT product";
RL Arch. Biochem. Biophys. 375:385-388(2000).
CC -!- FUNCTION: Methylates OH residues of flavonoid compounds. Substrate
CC preference is quercetin > myricetin >> luteolin. Dihydroquercetin
CC is not a substrate. Has an optimal pH of 7.5.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,5,7,3',4'-
CC pentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
CC 5,7,3',4'-tetrahydroxyflavone.
CC -!- ENZYME REGULATION: Does not require magnesium. Completely
CC inhibited by 5 mM of either NISO4 or p-chloromercuribenzoate
CC (pCMB).
CC -!- PATHWAY: Phenylpropanoid pathway.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
CC 2. COMT subfamily.

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CC or send an email to license@isb-sib.ch).

CC EMBL; U70424; AAB96879.1;
DR EMBL; AB013387; BAB11578.1;
DR EMBL; AY062837; AAL32915.1;
DR EMBL; AY081565; AAM10127.1;
DR EMBL; Z27062; CAAB1580.1;
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O.Methyltransf2.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF00891; Methyltransf_2; 1.
DR Methyltransferase; Transferase.
KW DOMAIN
FT 195 296 SAM-BINDING.
FT 229 229 D -> N (IN REF. 1).
FT CONFLICT 229 295 E -> V (IN REF. 4).
FT CONFLICT 295 295 E -> V (IN REF. 4).
FT CONFLICT 301 301 T -> S (IN REF. 4).
FT CONFLICT 348 348 V -> C (IN REF. 4).
SQ SEQUENCE 363 AA; 39616 MW; B4380028D89C43DC CRC64;

Query Match 20.7%; Score 390.5; DB 1; Length 363;
Best Local Similarity 30.0%; Pred. No. 3.8e-24;

```
DE Quercetin 3-O-methyltransferase 2 (EC 2.1.1.76) (Flavonol 3-O-
GN methyltransferase 2).
OS OMT2.
OC Chrysosplenium americanum (Golden saxifrage).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Saxifragaceae; Chrysosplenium.
OX NCBI_TaxID=36749;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Leaf;
RX MEDLINE=98181116; PubMed=9514654;
RA Gauthier A., Gullick P.J., Ibrahim R.K.;
RT "Characterization of two cDNA clones which encode O-methyltransferases
for the methylation of both flavonoid and phenylpropanoid
compounds.";
RL Arch. Biochem. Biophys. 351:243-249(1998).
CC -!- FUNCTION: Methylates OH residues of flavonoid and phenylpropanoid
compounds and shows a higher affinity for flavonoid than
phenylpropanoid substrates. Substrate preference is quercetin
(flavonoid) = luteolin (flavonoid) = 5-hydroxyferulic acid
(phenylpropanoid) > caffeic acid (phenylpropanoid) >> apigenin
(flavonoid) = kemferol (flavonoid). 3,4-dimethylquercetin is not
a substrate.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,5,7,3',4'-
pentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
5,7,3',4'-tetrahydroxyflavone.
CC -!- PATHWAY: Phenylpropanoid pathway.
CC -!- MISCELLANEOUS: The Vmax value for flavonoid compounds is two to
threefold lower for OMT2 than for OMT1.
CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
2. COMT subfamily.
CC -!- CAUTION: It is not sure if OMT1 and OMT2 are really encoded by two
different genes or if they represent cloning artifacts.
CC
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CC
CC EMBL; U16793; AAA86982.1; .
CC InterPro; IPR001601; Methyltransf.
CC InterPro; IPR001077; O_Metransf2.
CC InterPro; IPR000051; SAM_bind.
CC Pfam; PF00891; Methyltransf_2; 1.
CC Methyltransferase; Transferase.
CC DOMAIN
CC 173 274
CC SEQUENCE 343 AA; 37868 MW; 8D363A98330FDE4F CRC64;
Query Match 20.1%; Score 379; DB 1; Length 343;
Best Local Similarity 30.4%; Pred. No. 2,9e-23;
Matches 102; Conservative 68; Mismatches 131; Indels 34; Gaps 12;
QY 34 LKMWVELDIPDIHSHSHGQPTIFS--ELVSIQVFP-PTKTRQVQSLMRYLA;HNGFPEI 89
DQ 17 LKSAIELDLLEII-----RQDTCMSPTEIASHLPNTNPDPAMVDRIELLSQSVVTC 72
QY 90 VRIHDNIEAYALTAASELLVKSE--LSLAPMVEYFLEPNQCQAWNQ-----LKWVHEBDL 144
DQ 73 VRSVDDQRYGVLAPVCKYLTKNQDGVSTAAL-----C--LMNQDKVLMESVYHLKDA 122
QY 145 TV-----PEVSIQTPFDFPINKDRAYKSNFNEAMACDSQMLNLAFRDCNWFEGLESIVD 199
DQ 123 VLDGGIPNKAIGMSSEFVHGTDPRFNKVFNGKMSDHSHTITMKVFTQYVQGGTSLVD 182
QY 200 VGGGTGITAIIICEAPKPKLVLRPNVVENLSGNNLTFFVGMFKCIPKADAVLLKL 259
DQ 183 VGGGTGATLTMLSKYPIRCINFLDPLVIEDAPFPYGGIEHVGDMFVSPKGDIAIFMKW 242
QY 260 VLNWNDNDCKILENCKEASIGSEKTKGVVVIDTVINENKDERQVTELKLLMDV-HMAC 318
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Db 243 ICHDWSDEHCLKLLKNCYDAL---FNNGKVILAECLPEVPDSSLATKGWHIDVITVAH 299
QY 319 IINGKERKEEDWKLFMEAGFQSYKI--SPFTGYL 351
Db 300 NFGKERTKEFEALAKAAGFQGFQVFCNAFTYI 334

RESULT 11
COMT_CAPCH STANDARD; PRT; 359 AA.
AC 081646;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-
methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
GN COMT.
OS Capsicum chinense (Scotch bonnet) (Bonnet pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=80379;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Habanero;
RA Curry J., Mendoza M., O'Connell M.;
RT "Nucleotide sequence of a caffeic acid 3-O-methyltransferase gene from
Habanero Chile.";
RL (In) Plant Gene Register PGR98-170.
CC -!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to sinapic acid. The resulting
products may subsequently be converted to the corresponding
alcohols that are incorporated into lignins.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
cinnamate.
CC -!- PATHWAY: Lignin biosynthesis.
CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
2. COMT subfamily.
CC
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CC
CC EMBL; AF081214; AAC78475.1; .
CC InterPro; IPR001601; Methyltransf.
CC InterPro; IPR001077; O_Metransf2.
CC InterPro; IPR000051; SAM_bind.
CC Pfam; PF00891; Methyltransf_2; 1.
CC Lignin biosynthesis; Transferase; Methyltransferase.
CC SEQUENCE 359 AA; 39636 MW; 4A836904EF6D7119 CRC64;
Query Match 19.9%; Score 375.5; DB 1; Length 359;
Best Local Similarity 29.3%; Pred. No. 6e-23;
Matches 98; Conservative 67; Mismatches 124; Indels 45; Gaps 9;
QY 34 LKMWVELDIPDIHSHSHGQPTIFSILQVPTTKTRQVQSLMRYLAHNGFPEI 93
DQ 32 LKATVELDLEIMAKSGFGAFISFELAQL---PTKNPEAPVMI-----DRMFLIATY 83
QY 94 DNIEA-----YALTAASELLVKSE--LSLAPMVEYFLEPNQCQAWNQ-----L 135
DQ 84 SVLNCTLTLPDGRVERLYSLAPVCKFLTKNGDGVSTAPIL-----LMNQDKVLM 133
QY 136 KRWVHEBDLTV-----PEVSIQTPFDFPINKDRAYKSNFNEAMACDSQMLNLAFRDCN 190
DQ 134 ESWYHLDAVLDDGGVPFNKAYGMTTFEYHGTDPRFNKVFNGKMSDHTTSLMKKILEDTYG 193
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EMBL; X62096; CAA44006.1; -
EMBL; U13171; AB61731.1; -
PIR; S18558; S19568.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O.Methtransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf 2; 1.
Lignin biosynthesis; Transferase.
SEQUENCE 365 AA; 39805 MW; A6CEDEA4E0007CD CRC64;

Query Match	19.7%	Score 371.5;	DB 1;	Length 365;
Best Local Similarity	29.7%;	Pred. NO. 1.3e-22;		
Matches	97; Conservative	69; Mismatches 132;	Indels 29;	Gaps 8;

```

QY      QY      Db      QY      Db      QY      Db      QY      Db      QY      Db      QY      Db      QY      Db
34 LKWWVLDIPDIIHSHSGQPITFSELVSILQVPPTKR-----QVO$LMRYLAHN$GFF--877
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
36 LKTAIELDLLEIMAKAGP$AFLSTSEIASHL---PTKNPDAPWMLDRILLRLASYSILTC92
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
88 -----EIVRIHDNI$AYALTA$ELLVKSS$-LSLAPMWVEYFLEPNCOAQANQLKRW138
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
93 SLKDLPDGKVLERL-----YGLAPVCCKELTKNEDGVSVSPLCIMNQDKVLME$WYLYKDA146
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
139 VHEEDLTVFVESLGTFFDFINKDPAYNK$FN$EAACDSQMLNLAFRDCNWCVFEGL$SIV198
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
147 ILDGIP-FNKAYGMTAPEYHGTDPRFKVFNKGMSDHSTITWKILETYKFGEGLTSIV205
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
199 DVGGTGITAKIIEAFP$KLKCMVLERNNVNENL$GSNNLTFVGVDMPKCIPCADA$LLK258
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
206 DVGGTGA$VNTIYSKYPSIKGINFDLPHVEDAPSYPGVHVGGDMFVSV$PKADAVFMK265
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
259 LV$LHNWNDDCMKILENKEAI$GBSKTGKVVVIDTVINENKDERQVTELKLLMWHM-A317
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
266 WICHWD$HAHLCLKPLNCYDAL---PEN$KVI$LVCEILPV$PDTSLATKGVVHV$DVIMLA322
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
318 CIINGKERKEEDDWKLFWEAGFOSYKI344
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
323 HNP$GKERTETEKEFEGLAGAGFGQ$PEV349
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 14
COM1_POPKI
ID_COM1_POPKI STANDARD; PRT; 365 AA.
AC Q43046;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosyl-L-
methionine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (CAOMT-1).
GN HOMT1.
OS Populus kitakamiensis (Aspen).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid I; Malpighiales; Salicaceae; Populus.
OX NCBI_taxid=3698;
[1]
SEQUENCE FROM N.A.
RP Hayakawa T., Nanto K., Kawai S., Katayama Y., Morohoshi N.;
RT "Molecular cloning and tissue-specific expression of two genes that
RT encode caffeic acid O-methyltransferases from Populus kitakamiensis.";
RT Plant Sci. 113:157-165(1996).
CC -!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
CC and of 5-hydroxyferulic acid to sinapic acid. The resulting
CC products may subsequently be converted to the corresponding
CC alcohols that are incorporated into lignins.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
CC cinnamate.
CC -!- PATHWAY: Lignin biosynthesis.
CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
CC 2. COMT subfamily.

```

[illegible]

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```

CC ----- SAA08S58.1;
DR EMEL; D49710; SAA08S58.1;
DR Interbro; IPR001601; Methyltransf.
DR Interbro; IPR001077; O Methyltransf.
DR Interbro; IPR000051; SAM bind.
DR Pnam; PF00891; Methyltransf. 2; 1.
DR Lignin biosynthesis; Transfrase; Methyltransferase.
SQ Lignin biosynthesis; Transfrase; Methyltransferase.
SQ SCENESQUE 365 AA; 39791 MW; D6005B10FE5B83C CRC64;

```

Query Match 19.5%; Score 368.5; DB 1; Length 365;
Best Local Similarity 29.7%; Pred. No.2.e-22;
Matches 97; Conservative 68; Mismatches 133; Indels 29; Gaps 8;

[illegible]

RESULT 15
COMT_PRUDU
ID_COMT_PRUDU
STANDARD:
PRT: 365 AA.

Q43609;
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DT Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosyl-L-
DE methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
DE COMT.
GN
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OC NCBI_TaxID:3755;
OX [1] -
RN SEQUENCE FROM N.A.
RP
RC STRAIN=CV. Texas; TISSUE=Root;
RA Garcia-Has J., Messeguer R., Arus P., Puigdomenech P.;
RT "The caffeic acid O-methyltransferase from Prunus amygdalus.";
RL (In) Plant Gene Register PGR95-006.
CC -!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
CC and of 5-hydroxyferulic acid to sinapic acid. The resulting
CC products may subsequently be converted to the corresponding
CC alcohols that are incorporated into lignins.
CC CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
CC cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-

```

CC cinnamate.
CC -I- PATHWAY: Lignin biosynthesis.
CC -I- SIMILARITY: Belongs to the methyltransferase superfamily. Family
CC 2. COMT subfamily.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X83217; CAA58218.1; -
CC InterPro; IPR001601; Methyltransf.
CC InterPro; IPR001077; O Metransf2.
CC InterPro; IPR000051; SAM bind.
CC Pfam; PF00891; Methyltransf 2; 1.
CC Lignin biosynthesis; Transferase; Methyltransferase.
CC SEQUENCE 365 AA; 39762 MW; C8C4BFE7E0180E7 CRC64;
CC -----
Query Match      19.5%; Score 367.5; DB 1; Length 365;
Best Local Similarity 30.7%; Pred. No. 2.7e-22;
Matches 104; Conservative 65; Mismatches 133; Indels 37; Gaps 13;
QY 34 LKMWVLDIPDIHSHSHGQPIITFSELVSTLQVPPTKTR---QVQSLMRYLAHNGF--F 87
DB 36 LKAAIELDLLEIMAKAGPGVFLSPTDIASQI---PTKNPDAPVMDRMLRLLASYSILTY 92
QY 88 EIVRIHD-NIE-AYALTAASELLVKSE-LSLAPMVEYFLEPNCOGANQO---LKRWH 140
DB 93 SLRTADGKVERLYGLGPVCKFLTKNEBGVSIAPL-----C--LMNQDKVLLSESYH 142
QY 141 EEDLTV-----FEVSLGTPFDWDFINKDPAYNKSFEAMACDSQMLNLAERDCNWWVEGLE 195
DB 143 LKDAVEGGIPFNKAYGMTAFETHGTDPRFNKVFNRGMADHSTITWKKILETYKGEGLT 202
QY 196 SIVDVGGGTGITAKIIIEAFPPKLKCMVLERPNVVENLSGSSNNLTFFVGGDMFKCIPKADAV 255
DB 203 SVVDVGGGTGAVLNMIVSKYPSIKGINFDLPVIEDAPQYPGVEHVGDMFVSVPKGDAL 262
QY 256 LLKLVLHWNNDNCMKILENCKEAIISGESKTGKVVVIDTVINENKDBRQVTELKLLMDVH 315
DB 263 FMKICHDSDEHCLKFLKNCYAL---PDNGKVLGECILPVAPDSSLATRGVWHIDVI 319
QY 316 M-ACIINGKSKERKEDWKLFWEAGFQSYKI--SPFTGYL 351
DB 320 MLAHNPQKERTQEFPQALAKAGAGFQGFNVACSAFNTYV 358

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Search completed: November 10, 2003, 03:19:19
Job time : 25 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 58 VSILQVSSKIGNVRLMYLAHNGFFFIITKEE--ESYALTVASSELLVRGSDCLAPMV 115
 QY 121 EYFLEPNCQAWNOLKEWHEEDLTVEVSLGTFFWDFINKDPAYNKSFNEMACDSQML 180
 Db 116 ECVLDPTLSGSHYELKWIYEEDLTFGVTLGSGFDFDKNPEYNTSFNDVADASDKLI 175
 QY 181 NLAFRDCNWPEGLSIVDVGGGTGTAKIICEAPFKLKMVLERPNVVENLSSNNLTF 240
 Db 176 NLALRDCDFVFDGLSIVDVGGGTGTAKIICEAPFKLKMVLERPNVVENLSSNNLTF 235
 QY 241 VGGDMFKCIPKADAVLLKVLHNWDDCKMLNCKEASGESKTKGVVVDIVTINENK 300
 Db 236 VGGDMFTSIPNADAVLLKVLHNWDDCKMLNCKEASGESKTKGVVVDIVTINENK 295
 QY 301 DERQVTELKLMVHMVACIINGKERKEEDWKKLFMEAGFQSYKISPTGVLSLIEIYP 358
 Db 296 DENQVTLKLMVNMVAC-LNGKERNBEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP 352

RESULT 2
 O22308
 ID O22308 PRELIMINARY; PRT; 352 AA.
 AC O22308;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE 7-O-methyltransferase.
 GN 7-IOMT(6).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98145455; PubMed=9484461;
 RA He X.Z., Reddy J.T., Dixon R.A.;
 RT "Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning
 RT and characterization of an elicitor-inducible isoflavone 7-O-
 RT methyltransferase.";
 RL Plant Mol. Biol. 36:43-54 (1998).
 DR EMBL; U97125; AAC49928.1; -;
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR001077; O.Metransf2.
 DR Pfam; PF00891; Methyltransf_2; 1.
 KW Methyltransferase; Transferase.
 SQ SEQUENCE 352 AA; 39604 MW; 31B95226966C1C98 CRC64;

Query Match 68.3%; Score 1289; DB 10; Length 352;
 Best Local Similarity 67.9%; Pred. No. 3.1e-101;
 Matches 243; Conservative 56; Mismatches 53; Indels 6; Gaps 4;

QY 1 MASSLNCRKASELFOGQALLYKLLGFIDSKLKMVVELDIPDIHSHGHGPIITFSEL 60
 Db 1 MASSI-NGRKESEIFKAQALLYKHIFADISMSLKWAVENMIPNII--QNHGKPSISNL 57
 QY 61 VSILQVPTKTRQVQSLMRYLAHNGFFFIIVRIHNIAYALTAASELLVKSSELAPMV 120
 Db 58 VSILQVSSKIGNVRLMYLAHNGFFFIITKEE--ESYALTVASSELLVRGSDCLAPMV 115
 QY 121 EYFLEPNCQAWNOLKEWHEEDLTVEVSLGTFFWDFINKDPAYNKSFNEMACDSQML 180
 Db 116 ECVLDPTLSGSHYELKWIYEEDLTFGVTLGSGFDFDKNPEYNTSFNDVADASDKLI 175
 QY 181 NLAFRDCNWPEGLSIVDVGGGTGTAKIICEAPFKLKMVLERPNVVENLSSNNLTF 240
 Db 176 NLALRDCDFVFDGLSIVDVGGGTGTAKIICEAPFKLKMVLERPNVVENLSSNNLTF 235
 QY 241 VGGDMFKCIPKADAVLLKVLHNWDDCKMLNCKEASGESKTKGVVVDIVTINENK 300
 Db 236 VGGDMFTSIPNADAVLLKVLHNWDDCKMLNCKEASGESKTKGVVVDIVTINENK 295
 QY 301 DERQVTELKLMVHMVACIINGKERKEEDWKKLFMEAGFQSYKISPTGVLSLIEIYP 358
 Db 296 DENQVTLKLMVNMVAC-LNGKERNBEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP 352

Db 296 DENQVTLKLMVNMVAC-LNGKERNBEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP 352

RESULT 3
 O24529
 ID O24529 PRELIMINARY; PRT; 352 AA.
 AC O24529;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Isoflavone-O-methyltransferase.
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98145455; PubMed=9484461;
 RA He X.Z., Reddy J.T., Dixon R.A.;
 RT "Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning
 RT and characterization of an elicitor-inducible isoflavone 7-O-
 RT methyltransferase.";
 RL Plant Mol. Biol. 36:43-54 (1998).
 DR EMBL; U97125; AAC49928.1; -;
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR001077; O.Metransf2.
 DR Pfam; PF00891; Methyltransf_2; 1.
 KW Transferase.
 SQ SEQUENCE 352 AA; 39603 MW; 31B95228986C1296 CRC64;

Query Match 68.1%; Score 1285; DB 10; Length 352;
 Best Local Similarity 67.6%; Pred. No. 6.7e-101;
 Matches 242; Conservative 57; Mismatches 53; Indels 6; Gaps 4;

QY 1 MASSLNCRKASELFOGQALLYKLLGFIDSKLKMVVELDIPDIHSHGHGPIITFSEL 60
 Db 1 MASSI-NGRKESEIFKAQALLYKHIFADISMSLKWAVENMIPNII--QNHGKPSISNL 57
 QY 61 VSILQVPTKTRQVQSLMRYLAHNGFFFIIVRIHNIAYALTAASELLVKSSELAPMV 120
 Db 58 VSILQVSSKIGNVRLMYLAHNGFFFIITKEE--ESYALTVASSELLVRGSDCLAPMV 115
 QY 121 EYFLEPNCQAWNOLKEWHEEDLTVEVSLGTFFWDFINKDPAYNKSFNEMACDSQML 180
 Db 116 ECVLDPTLSGSHYELKWIYEEDLTFGVTLGSGFDFDKNPEYNTSFNDVADASDKLI 175
 QY 181 NLAFRDCNWPEGLSIVDVGGGTGTAKIICEAPFKLKMVLERPNVVENLSSNNLTF 240
 Db 176 NLALRDCDFVFDGLSIVDVGGGTGTAKIICEAPFKLKMVLERPNVVENLSSNNLTF 235
 QY 241 VGGDMFKCIPKADAVLLKVLHNWDDCKMLNCKEASGESKTKGVVVDIVTINENK 300
 Db 236 VGGDMFTSIPNADAVLLKVLHNWDDCKMLNCKEASGESKTKGVVVDIVTINENK 295
 QY 301 DERQVTELKLMVHMVACIINGKERKEEDWKKLFMEAGFQSYKISPTGVLSLIEIYP 358
 Db 296 DENQVTLKLMVNMVAC-LNGKERNBEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP 352

RESULT 4
 O22555
 ID O22555 PRELIMINARY; PRT; 343 AA.
 AC O22555;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE O-methyltransferase.
 GN IOMT2003.
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

QY 125 EPNCGANQLKRWVHEEDLTVEVSLGTPFWDFTINKDPAYNKSFNEMACDSQML-NLA 183
 Db 133 DVLNPNWYLSLTFQNDPTTDFDTHAGTWFWDYGNHQPSIAHLFNDAMASDARLVTSVI 192
 QY 184 FRDCNWFEGLESIVDVGGGTGTAKIICEAPPKLCMWLERPNVVENLSGNNLTFVGG 243
 Db 193 INDCGVFEGLESVDVGGGTGTAKIADAPPHIECTVLDLPHVVDLQSKNLKYTGG 252
 QY 244 DMFKCIPKADAVLLKLVLHWNNDCKMILENCKEAIKSGESKTGVVVIDTVINENKDER 303
 Db 253 DMFEAVPPADTVLLKWLHWDSECEIKILRSRVAITGKKGKGVIIIDMMWENQKGE 312
 QY 304 QVTELKLLMDVHMCIINGKERKEEDWKKLFMEAGFQSKISPTFGYLSLIEIYP 358
 Db 313 ESIEITQLFFDMLMALVGGKERNKEWAKLFTDAGFSDYKITPISGLRSLIEVYP 367

RESULT 7

Q8GU24 PRELIMINARY; PRT; 367 AA.
 AC Q8GU24;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Orcinol O-methyltransferase.
 GN OOMT1.

OS Rosa chinensis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
 OX NCBI_TaxID=74649;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=sv. Old Blush;

RA Cock J.Mark, Scalliet G., Huguency P.;

RT "Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ439741; CND29458.1; -
 KW Transferase; Methyltransferase.
 SQ SEQUENCE 367 AA; 41278 MW; 9739F3B2D09FEF7C CRC64;

Query Match 45.8%; Score 863; DB 10; Length 367;

Best Local Similarity 46.2%; Pred. No. 58-65;

Matches 164; Conservative 68; Mismatches 119; Indels 4; Gaps 3;

QY 6 NNGKASEIFQOQALLYKHLGFIIDSCKLKMVELDIPDIHSHGHGQPIPFSELVSILQ 65
 Db 15 SNGEHSNELLHAQAHWNHIFSPFINSMSLSKSAIQLGIPDII--NKGYPMTLSLTSALP 72
 QY 66 VPPTKTQVQSLMRYLAHNGFFEIFVRI-HDNEAYALTAASELLVKSELSLAPMVEYFL 124
 Db 73 IHPTKSHSVYRLMRLVHSGFFAKKLSKTDDEGYTLTDSQLLKHDPPLSLTPYLTA 132

QY 125 EPNCGANQLKRWVHEEDLTVEVSLGTPFWDFTINKDPAYNKSFNEMACDSQML-NLA 183
 Db 133 DVLNPNWYLSLTFQNDPTTDFDTHAGTWFWDYGNHQPSIAHLFNDAMASDARLVTSVI 192

QY 184 FRDCNWFEGLESIVDVGGGTGTAKIICEAPPKLCMWLERPNVVENLSGNNLTFVGG 243
 Db 193 INDCGVFEGLESVDVGGGTGTAKIADAPPHIECTVLDLPHVVDLQSKNLKYTGG 252
 QY 244 DMFKCIPKADAVLLKLVLHWNNDCKMILENCKEAIKSGESKTGVVVIDTVINENKDER 303
 Db 253 DMFEAVPPADTVLLKWLHWDSECEIKILRSRVAITGKKGKGVIIIDMMWENQKGE 312

QY 304 QVTELKLLMDVHMCIINGKERKEEDWKKLFMEAGFQSKISPTFGYLSLIEIYP 358
 Db 313 ESIEITQLFFDMLMALVGGKERNKEWAKLFTDAGFSDYKITPISGLRSLIEVYP 367

RESULT 8

Q8L5K7 PRELIMINARY; PRT; 366 AA.
 AC Q8L5K7;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Orcinol O-methyltransferase.
 GN OOMT2.

OS Rosa hybrid cultivar.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

OX NCBI_TaxID=128735;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=fc0895;

RA MEDLINE=22167322; PubMed=12177504;

RA Lavid N., Wang J., Shalit M., Guterman I., Bar E., Beuerle T.,

RA Menda N., Shafir S., Zamir D., Adam Z., Vainstein A., Weiss D.,

RA Pichersky E., Lewinsohn E.;

RT "O-methyltransferases involved in the biosynthesis of volatile phenolic derivatives in rose petals.";

RL Plant Physiol. 129:1899-1907(2002).

DR EMBL; AF502434; AAM23005.1; -

DR InterPro; IPR001601; Methyltransf.

DR InterPro; IPR001077; O.Metransf2.

DR InterPro; IPR000051; SAM bind.

DR Pfam; PF00891; Methyltransf. 2; 1.

KW Transferase; Methyltransferase.

SQ SEQUENCE 366 AA; 41226 MW; CAF4E17D3230D29E CRC64;

Query Match 44.9%; Score 847.5; DB 10; Length 366;

Best Local Similarity 45.6%; Pred. No. 1e-63;

Matches 162; Conservative 67; Mismatches 121; Indels 5; Gaps 3;

QY 6 NNGKASEIFQOQALLYKHLGFIIDSCKLKMVELDIPDIHSHGHGQPIPFSELVSILQ 65

Db 15 SNGEHSNELLHAQAHWNHIFSPFINSMSLSKSAIQLGIPDIIKHG---PMTLSLTSALP 71

QY 66 VPPTKTQVQSLMRYLAHNGFFEIFVRI-HDNEAYALTAASELLVKSELSLAPMVEYFL 124

Db 72 IHPTKSHSVYRLMRLVHSGFFAKKLSKTDDEGYTLTDSQLLKHDPPLSLTPYLTA 131

QY 125 EPNCGANQLKRWVHEEDLTVEVSLGTPFWDFTINKDPAYNKSFNEMACDSQML-NLA 183

Db 132 DVLNPNWYLSLTFQNDPTTDFDTHAGTWFWDYGNHQPSIAHLFNDAMASDARLVTSVI 191

QY 184 FRDCNWFEGLESIVDVGGGTGTAKIICEAPPKLCMWLERPNVVENLSGNNLTFVGG 243

Db 192 IDCKGVFEGLESVDVGGGTGTAKIADAPPHIECTVLDLPHVVDLQSKNLKYTGG 251

QY 244 DMFKCIPKADAVLLKLVLHWNNDCKMILENCKEAIKSGESKTGVVVIDTVINENKDER 303

Db 252 DMFEAVPPADTVLLKWLHWDSECEIKILRSRVAITGKKGKGVIIIDMMWENQKGE 311

QY 304 QVTELKLLMDVHMCIINGKERKEEDWKKLFMEAGFQSKISPTFGYLSLIEIYP 358

Db 312 ESIEITQLFFDMLMALVGGKERNKEWAKLFTDAGFSDYKITPILGLRSLIEVYP 366

RESULT 9

Q8GU23 PRELIMINARY; PRT; 366 AA.
 AC Q8GU23;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Orcinol O-methyltransferase.
 GN OOMT2.

OS Rosa chinensis.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Matches	159;	Conservative	66;	Mismatches	123;	Indels	4;	Gaps	3
QY	9	RKASEIFQGOALLYGHLGFI	DSKCLKMWV	ELDIPDI	IHSHSQPITF	SELVSILOVPP	68		
Db	5	RASHELLQAQAHYHWFIS	INSLSLKCAV	QOLDIPDVI	--QKHQPMTL	SELVSALPISP	62		
QY	69	TKTROVQSLMRYLAHNGF	FFIVRIHD	--NIEFAYAL	TAASELLVK	SELSLAPWVEYFLEPN	127		
Db	63	TKAHFTPLRMRIIVHSG	FFAKESLSG	CGEOGYILT	DSALLKKNP	WSARDFLLAMLSP	122		
QY	128	COGAMNOLKEWHEEDLT	VFEVSLGT	PFDFPINK	DPAYKNSF	NEAMACDSQML--NLAFRD	186		
Db	123	LTPDQYQLTWTFQNDP	PTPHVNGMT	CTWYVNO	DPFLAHFF	NADAMASDAQLI	SSLVDD	182	
QY	187	CNNVFFGLEISIVDVG	GGTGITAK	IICBAFPL	KCMVLERP	NVVENLSGSNNLT	FYGGDMF	246	
Db	183	CKEVFGVDSLVDVGG	TGTVAKSI	ADAFPHM	KCTVLDL	PHVADLKG	SKNLEYVAGDMF	242	
QY	247	KCTPKADAVLLKLVL	HNWNDCK	ILNCKE	ALSGESK	TGKVVVIV	DTVINENKDERQVT	306	
Db	243	EAVPAADAIEFLK	WILHDWS	DEBCKIL	ERCKAAV	TREGKKGK	IVIVEMTVENKNTDKESG	302	
QY	307	ELKLLMDVHMACI	INGKREKE	EDWKLF	MEBAGF	OSYKISPT	FGYLSLIEIYP	358	
Db	303	ETQLFFDMHMMV	STGKERNE	KEWAKLF	SAGFSQY	KIITPL	FGFKSLIEIYP	354	
RESULT	11								
Q8GU21		PRELIMINARY;							
ID	Q8GU21								
AC	Q8GU21								
DT	01-MAR-2003	(T-EMBLrel. 23, Created)							
DT	01-MAR-2003	(T-EMBLrel. 23, Last sequence update)							
DT	01-MAR-2003	(T-EMBLrel. 23, Last annotation update)							
DE	Orcinol O-methyltransferase (Fragment).								
GN	COMT4.								
OS	Rosa hybrid cultivar.								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;								
OC	eurosid 1; Rosales; Rosaceae; Rosoideae; Rosa.								
OX	NCBI_TaxID=128735;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=cv. Lady Hillington;								
RA	Cock J.Mark, Scalliet G., Huguency P.;								
RT	"Characterisation of a novel O-methyltransferase involved in the								
RT	biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two								
RT	major scent components of rose flowers.";								
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AJ439744; CAD29556.1; --								
KW	Transferase; Methyltransferase.								
FT	NON_TER	1							
FT	NON_TER	348							
FT	NON_TER	348							
SQ	SEQUENCE	348 AA;	38982 MW;	24391E70	DDB33C09	CEC64;			
Query Match									
Best Local Similarity									
Matches	158;	Conservative	67;	Mismatches	115;	Indels	8;	Gaps	4;
QY	6	NNGEKASEIPQGOALLYKHL	GLGFI	DSKCLKMWV	ELDIPDI	IHSHSQPITF	SELVSILOQ	65	
Db	5	SNGEHSNELHAQAHWHIF	SFINSLSKAI	OLGIPDII	--NKHGYPMTL	SELSSALP	62		
QY	66	VPTTKTRQVQSLMRYLAH	NGIFF--	--ETVR	THDNTAE	VALTAASELL	VKSSSELSLAPWVEY	122	
Db	63	IHPKSHSVRLMRLIIVH	SSEGF	FAKKLSK	IDE--	--EGVTL	DSQLLKHDP	LSLTPFLTA	120
QY	123	FLFPCOGANQLKRWV	HEEDLT	VFEVSLGT	PFDFPINK	DPAYKNSF	NEAMACDSQML--N	181	
Db	121	MLDPVLTKPNYLS	TWFQND	PTPFDT	THGWT	FDYGNHQP	NIHAELFN	DAMASDARLVT	180
QY	182	LAFRDCNNWFEGL	ESIVDVG	GGTGITAK	IICEAPFK	LKCMVLERP	NVVENLSGSNNLT	FTV	241

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Db 181 VIIDCKGVFEGLSLVDVGGTGTAKAIAADAPPHIECTVLDLPHVVGDIQGSKNLYKT 240
Qy 242 GDMFKCIPKADAVLLKVLHNNWDCMKILENCKEASIGESKTGKVVVDITVINENKD 301
Db 241 GDMFEAVPPADTVLLKWLHNDWDECIKILKRSVAITSKDKKGVIIIDMMWENQKG 300
Qy 302 EQVTEKLKLDVHMVMAACIINGKERKEEDWKLFMEAGFSQYKISPFPTG 349
Db 301 DEESIEIQLFLDMLMVALVGKERNKEWAKLFTDAGFSYKITPILG 348

RESULT 12
Q8GU22 PRELIMINARY; PRT; 348 AA.
AC Q8GU22;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Orcinol O-methyltransferase (Fragment).
GN OOMT3.
OS Rosa hybrid cultivar.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
OX NCBI_TaxID=128735;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lady Hillington;
RA Cock J. Mark, Scalliet G., Huguency P.;
RT "Characterisation of a novel O-methyltransferase involved in the
RT biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two
RT major scent components of rose flowers.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439743; CAD29555.1; -.
KW Transferase; Methyltransferase.
FT NON TER 1
FT NON TER 348 348
SQ SEQUENCE 348 AA; 39034 MW; 0AFD4D325A0DBB1D CRC64;

Query Match 43.3%; Score 817; DB 10; Length 348;
Best Local Similarity 45.1%; Pred. No. 3.8e-61;
Matches 156; Conservative 67; Mismatches 119; Indels 4; Gaps 3;

Qy 6 NNGRKASIFQOQALLYKHLLGFDISKCLKWVVDIPDIHSHSHGQIPITFSELVSLQ 65
Db 5 SNGEHSNELLHAQAHWNHIFSFINSMSLKSAIQLGIPDII--NKYGYPTLSLTSALP 62
Qy 66 VPPTKTROVQSLMRYLAHNGFPEIVRI--HDNIEAYALTAASELLVKSELSLAPVVEYL 124
Db 63 IHPTKSHSVYRLMRILVHSGFFAKKLSKTDBEGYTLTDAQSLLKDPPLSLTPYLTAML 122
Qy 125 EPNCGAWNQLKRWVHEEDLTVEVSLGTPFDWDFINKDPAYNKSFNEMACDSQML-NLA 183
Db 123 DFVLTNPWNYLSTFQNDPTPFDTFAHGWTWYGNHQPSTIAHLFDNADWASDARLVTSVI 182
Qy 184 FRDCNWVFEGLSIVDVGSGGTITAKIICEAPFKLKMVLERNPVNENLGSNNLTFVGG 243
Db 183 IDDCGVFEGLSIVDVGSGGTGTAKAIAADAPPHIECTVLDLPHVVDLQGSKNLYKTGG 242
Qy 244 DMFKCIPKADAVLLKVLHNNWDCMKILENCKEASIGESKTGKVVVDITVINENKDER 303
Db 243 DMFEAVPPADTVLLKWLHNDWDECIKILKRSVAITSKDKKGVIIIDMMWENQKGD 302
Qy 304 QVTEKLKLDVHMVMAACIINGKERKEEDWKLFMEAGFSQYKISPFPTG 349
Db 303 ESIEIQLFLDMLMVALVGKERNKEWAKLFTDAGFSYKITPILG 348

RESULT 13
Q65859 PRELIMINARY; PRT; 356 AA.
ID Q65859
AC Q65859;
DT 01-AUG-1998 (Tremblrel. 07, Created)

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DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE O-methyltransferase.
OC Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Texas;
RA Suelves M., Puigdomenech P.;
RT "Specific mRNA accumulation of a gene coding for an O-
RT methyltransferase in almond (Prunus amygdalus, Batsch) flower
RT tissues.";
RL Plant Sci. 134:79-88(1998).
DR EMBL; AJ223151; CAA11131.1; -.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O-Metransf2.
DR Pfam; PF00891; Methyltransf_2; 1.
KW Methyltransferase; Transferase.
SQ SEQUENCE 356 AA; 40206 MW; 4CC6F169513F4EA9 CRC64;

Query Match 40.1%; Score 757; DB 10; Length 356;
Best Local Similarity 42.3%; Pred. No. 4.8e-56;
Matches 151; Conservative 70; Mismatches 130; Indels 6; Gaps 4;

Qy 5 LNNRKASIFQOQALLYKHLLGFDISKCLKWVVDIPDIHSHSHGQIPITFSELVSL 64
Db 3 LSNEMSANLLHAQAHWNHIFSFINSMSLKCAVQLGIPDII--KKHGNPMSLDLISAL 60
Qy 65 QVPPTKTROVQSLMRYLAHNGFPEIVRIH--DNIEAYALTAASELLVKSELSLAPVVEY 122
Db 61 PIHPKXSNVCYRLMRILVHSGFFCRQKLSBELDEEGYVLTDASELLKDDPLSARPLFG 120
Qy 123 FLBNPCQGANQLKRWVHEEDLTVEVSLGTPFDWDFINKDPAYNKSFNEMACDSQMLN- 181
Db 121 ALDPFMTKPHYPTFWFQNDPTACVTAHGTTFWDFCLESLSHIENDAMASDARLSK 180
Qy 182 LAFRDCNWVFEGLSIVDVGSGGTITAKIICEAPFKLKMVLERNPVNENLGSNNLTFV 241
Db 181 VSNEXYKGVFEGLSIVDVGSGGTGTAKAIAADVFPVVECTVFDLPHVVDLQGSNLYKFF 240
Qy 242 GDMFKCIPKADAVLLKVLHNNWDCMKILENCKEASIGESKTGKVVVDITVINENKD 301
Db 241 GDMFEAVPPADTVLLKWLHNDWDECIKILKRSVAITRKEKKGKGVIIIDMMWENQKGD 300
Qy 302 EQVTEKLKLDVHMVMAACIINGKERKEEDWKLFMEAGFSQYKISPFPTGYSLSLIEIYP 358
Db 301 DQSI-ETQLFPDMLMVALVGKERNKEWAKLFSAGFSYKITPILGLYLYIEVYP 356

RESULT 14
Q93WU2 PRELIMINARY; PRT; 357 AA.
ID Q93WU2;
AC Q93WU2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Eugeniol O-methyltransferase.
OS Ocimum basilicum (sweet basil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Ocimum.
OX NCBI_TaxID=39350;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. EMX-1; TISSUE=Peltate glandular trichome;
RA Gang D.R., Lavid N., Zubieta C., Chen F., Beuerle T., Lewinsohn E.,
RA Noel J.P., Fichersky E.;
RT "Characterization of Phenylpropane O-Methyltransferases from Sweet
RT Basil: Facile Change of Substrate Specificity and Convergent Evolution
RT within a Plant OMT Family.";

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RL Plant Cell 0:0-0(2002).
DR EMBL; AF435008; AAL30424.1; -.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR001077; O-Methyltransf.
DR InterPro; IPR000051; SAM_Bind.
DR Pfam; PF00891; Methyltransf_2; 1.
KW Methyltransferase; Transferase.
SQ SEQUENCE 357 AA; 40236 MW; FC050C48BF6D719C CRC64;

Query Match
Best Local Similarity 38.5%; Score 734; DB 10; Length 357;
Matches 145; Conservative 75; Mismatches 121; Indels 8; Gaps 5;

QY 13 EIFQGALLKHLIGFIDSKLKWMLDIPDIHSHSHGQPIITFSSILVSILOVPPKTR 72
DB 14 QLLQAOVHVHMYAFANSLKCAIQIGIPDIH--HKHGRPTLSQLQSIPIKKEKTQ 71
QY 73 QVQSLMYLAHNGFFEIVRIHNDIE-AVALTAASELLVKSSELSLAPWVEYFLEPNCOGA 131
DB 72 CFQRLMALVNSNFFIEBNSNNOVCVWLTTPASCLLKEAPLTAVTFLVQVLDPTFNP 131
QY 132 WNQLKRW-VHEEDLTVEVSLGTFFWDPINKDPAYNKSFNEMACDSQMLNLAFL-RDCNW 189
DB 132 WHHMSWFTHKHAQTPEAANGCTFWKLANEPKGRFFDEANSCSKLIAHVFTKDKYH 191
QY 190 VFEGLSEIVDVGSGTGITAKIICEAFPKLKWLERPNVWENLGSNNLTFVGGDMFKCI 249
DB 192 VIEGIRLVDVGGNGTWAKAIVAMPTIKTVTIDLPVAVAGLESTDLNLTIGGDMFQSI 251
QY 250 PKADAVLLKLVHNNWDCMKILENCKEALSGSKTKGVVVDVTVINENKDERQVTELK 309
DB 252 PSADAILLKSIIHDWDDVEGLKILKCKDAV---VMGKVIIDVWGVNHDIDEVLEDQ 308
QY 310 LLMVDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPTGYLSLIEIYP 358
DB 309 LHPDMAMCYFNAKERTMSEWEKLIYDAGFKSYKLTLPAGVRSLEIAYP 357

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Job time : 110 secs
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RESULT 15

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Q8GSNO PRELIMINARY; PRT; 347 AA.
AC Q8GSNO;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE O-methyltransferase.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Gentianales; Apocynaceae; Rauvolfiaceae; Vinceae;
OC Catharanthus
OX NCBI_taxid=4058;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22371605; PubMed=12482447;
RA Cacace S., Schroeder G., Wehinger E., Strack D., Schmid J.,
RA Schroeder J.;
RT "A flavonol O-methyltransferase from Catharanthus roseus performing
RT two sequential methylations."
RL Phytochemistry 62:127-137(2003).
DR EMBL; AY127569; AAM97498.1; -.
KW Transferase; Methyltransferase.
SQ SEQUENCE 347 AA; 38789 MW; 7PB24AC0BC97AB35 CRC64;

Query Match
Best Local Similarity 38.5%; Score 726.5; DB 10; Length 347;
Matches 148; Conservative 73; Mismatches 117; Indels 17; Gaps 8;

QY 10 KASEIFQGOALLKHLIGFIDSKLKWMLDIPDIHSHSHGQPIITFSSILVSILOVPPPT 69
DB 4 ETAETRKAAQAYSRHVSFVSTSLCKLAIQLEIPEAI--HNHGKPTLSDLTNSLPINFS 61
QY 70 KTRQVQSLMYLAHNGFFEIVRIHNDIEAYALTAASELLVKSSELSLAPWVEYFLEPN-- 127
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 23:30:19 ; Search time 4620 seconds
(without alignments)
10271.681 Million call updates/sec

Title: US-09-868-547-3

Perfect score: 1160

Sequence: 1 gtttgctattatggcttctt.....ataaaagtattcttgggtt 1160

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hhg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
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- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_ats.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_hhg_hum.*
- 31: em_hhg_inv.*
- 32: em_hhg_other.*
- 33: em_hhg_mus.*
- 34: em_hhg_pln.*
- 35: em_hhg_rod.*
- 36: em_hhg_mam.*
- 37: em_hhg_vrt.*
- 38: em_sy.*
- 39: em_hhg_hum.*
- 40: em_hhg_mus.*
- 41: em_hhg_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	697.8	60.2	1121	8	AB091685	AB091685 Glycyrthi
2	647	55.8	1284	8	MSAP000975	AF000975 Medicago
3	645.4	55.6	1231	6	AX050436	AX050436 Sequence
4	645.4	55.6	1231	6	MSD09125	U97125 Medicago sa
5	642.2	55.4	1227	8	MSAP000976	AF000976 Medicago
6	594.2	51.2	1194	8	AF023481	AF023481 Medicago
7	337.6	29.1	1349	8	AB091684	AB091684 Glycyrthi
8	321.6	27.7	1337	8	PSU69554	U69554 Pisum sativ
9	318.8	27.5	111587	2	AC136140	AC136140 Medicago
10	318	27.4	1363	8	AB091686	AB091686 Lotus jap
11	305.6	26.3	1257	8	PAU082011	U82011 Prunus arme
12	302.8	26.1	1253	8	AF502434	AF502434 Rosa hybr
13	302.8	26.1	1265	8	RCH439742	AJ439742 Rosa chin
14	302.4	26.1	1252	8	AF502433	AF502433 Rosa hybr
15	302.4	26.1	1275	8	RCH439741	AJ439741 Rosa chin
16	287.6	24.8	1043	8	RHY439744	AJ439744 Rosa hybr
17	286	24.7	1043	8	RHY439743	AJ439743 Rosa hybr
18	274.2	23.6	1218	8	PAJ3151	AJ22151 Prunus am
19	209.2	18.0	1041	6	E28578	E28578 Norococclauri
20	209.2	18.0	1267	8	D29811	D29811 Coptis japo
21	206	17.8	1071	8	AF435007	AF435007 Ocimum ba
22	205.6	17.7	1074	8	AF435008	AF435008 Ocimum ba
23	195	16.8	83007	8	AC123575	AC123575 Medicago
24	180.4	15.6	1280	8	D29812	D29812 Coptis japo
25	179.8	15.5	112530	2	AC140068	AC140068 Medicago
26	178.4	15.4	1050	6	E27546	E27546 (s)-3'-Hydr
27	152.2	13.1	1402	8	HVOME1	X77467 H.vulgare L
28	147.4	12.7	1354	8	AB014456	AB014456 Pyrus pyr
29	146.8	12.7	1659	8	AX127568	AX127568 Catharant
30	146.6	12.6	1279	8	PTU39301	U39301 Pinus taeda
31	144.8	12.5	1703	8	AX127569	AX127569 Catharant
32	142	12.2	1268	8	MZBOMT	L14063 Zea mays O-
33	131.6	11.3	1378	8	AB073908	AB073908 Coptis ja
34	131	11.3	1421	8	PRU70873	U70873 Pinus radia
35	130	11.2	1396	8	AF239740	AF239740 Vitis vin
36	125.8	10.8	1503	8	AF212316	AF212316 Capsicum
37	124.2	10.7	1377	8	CAU083789	U83789 Capsicum an
38	122.2	10.5	951	6	AX660124	AX660124 Sequence
39	121	10.4	1469	8	AF064694	AF064694 Thalictru
40	119.4	10.3	1306	8	AF064695	AF064695 Thalictru
41	119.2	10.3	1316	8	AF064693	AF064693 Thalictru
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43	119.2	10.3	1458	8	TAU76384	U76384 Triticum ae
44	118	10.2	1098	6	AX259373	AX259373 Sequence
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ALIGNMENTS

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LOCUS	Glycyrthiza echinata	Glycyrthiza echinata	D70MT	mRNA for S-adenosyl-L-methionine:		
DEFINITION	daidzein 7-O-methyltransferase, complete cds.					
ACCESSION	AB091685					
VERSION	AB091685.1	GI:28804593				
KEYWORDS	Glycyrthiza echinata					
SOURCE	Glycyrthiza echinata					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Galegeae;					
	Glycyrthiza.					
REFERENCE	1					

Akashi, T., Sawada, Y., Shimada, N., Sakurai, N., Aoki, T. and Ayabe, S.
 cDNA cloning and biochemical characterization of
 s-adenosyl-L-methionine: 2,7,4'-trihydroxyisoflavanone
 4'-O-methyltransferase, a critical enzyme of the legume
 isoflavonoid phytoalexin pathway
 Plant Cell Physiol. 44 (2), 103-112 (2003)
 22497945
 MEDLINE
 PUBMED
 12610212
 2 (bases 1 to 1121)
 Authors
 Akashi, T., Aoki, T. and Ayabe, S.
 Direct Submission
 Submitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University,
 Department of Applied Biological Sciences; Kameino 1866, Fujisawa,
 Kanagawa 252-8510, Japan E-mail: ayabe@rs.nihon-u.ac.jp,
 Tel: 81-466-84-3703, Fax: 81-466-80-1141
 Location/Qualifiers
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 RAASELVGSELCLAPMVECDLPTLSGSHQKXWYEDDLTFGVSLGSHWFLN
 ENPEYKSFNDAMASDSQMINIALRDCNSGFEFVESIVDVGGIGITAKIIIDTPPNL
 KCVIFDRPKVNLGTNNLSVYGVGMFQSPKADAVLLKWLHNWTDNDCRILEK
 KEAVSDGKGVIIIEVMINENQDEHEITGTIKLLMDVNMACLNGKRSBEBWKLFI
 EAGPRDYKISPTGTLSLIEVY"
 339 a 210 c 267 g 305 t
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 ORIGIN
 Query Match 60.2%; Score 697.8; DB 8; Length 1121;
 Best Local Similarity 80.1%; P-red. No. 3.2e-148;
 Matches 864; Conservative 0; Mismatches 197; Indels 18; Gaps 3;
 QY 18 CTTCAATTAACCAATGCGCTTAAGCAAGTCAGATTTTCAAGTCAAGCTCTCTGTGACA 77
 DB 52 CTTCTTCAATCAATGCGGCGCAACCAAGTCAGATCTTCAAGGCCAGGCTCTCTGTGACA 111
 QY 78 AACATTGCTTGGCTTCATAGATCTTAAGTGCTCAAAATGGATGGTTGAGCTTGACATAC 137
 DB 112 GACACATATACGCCCTTCATAGATCTCAATGCTGCTGAATGGATGCTGTGAGCTAGACATAC 171
 QY 138 CGACATAATCCACAGCCATAGCCATGGCCAAACCCATTACTTTTCAGAGTTGGTGTCAA 197
 DB 172 CAAACATAATCCAC-----AACCATGGAAACCCATTACTGTTTCAGAGTTGGTGTCAA 225
 QY 198 TTCTCAAGTCCACCAACTAAACTCGTCAGTGCAGAGCCATCAGCTTATCTAGCAC 257
 DB 226 TCGTAAAGTTCCACAAACCAAGCTGGGAACGTGCAGCGGTATCATGCGGTACATGGCAC 285
 QY 258 ACAATGGATTCTTTGAGATAGTAGAATC-----CATGACACATAGAGCATATG 308
 DB 286 ACAATGGTTCTTTGAGAGAGTGAATCCAGAGAGCGCAGAGAGAGAGAGCATATG 345
 QY 309 CTCTCACTGCTGCTTCAGAGTTACTTGTCAAAAGCAGTGTAGCTTAGTTCCTCAATGG 368
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 DB 406 TTGAGTGTGTTCTTGACCACTCTCTCAGGTTTCATACCATCAGCTCAAGAGTGGATCT 465

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 QY 729 TTGCTGTGGGACATGTTTAAATGCAATCCCAAGGCTGATGCGAGTTCTGCTTAAGTTGG 788
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 QY 849 TTTCAGGTGAAAGCAAAACAGGAAAGTAGTTGTCAATAGATCTGTGATATAACGAAACA 908
 DB 886 TTTCAAGTGTGGGAAAGGAAAGAGTAATTTATTATAGAAATGGTGTGATAAATAAGAAATC 945
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 DB 946 AGGATGAGCATGAATCACTCTGGAACAAAGCTCTTTGATGATGATGATGATGATGATGATG 1002
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 DB 1003 TTAATGGAAG 1062
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 LOCUS Medicago sativa 7-O-methyltransferase (7-IOMT(6)) mRNA, complete cds.
 DEFINITION
 ACCESSION AF000975 GI:2580581
 VERSION AF000975.1
 KEYWORDS Medicago sativa
 SOURCE Medicago sativa
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; Magnoliopsida; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 1284)
 AUTHORS He, X.Z., Reddy, J.T. and Dixon, R.A.
 TITLE Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone 7-O-methyltransferase
 JOURNAL Plant Mol. Biol. 36 (1), 43-54 (1998)
 MEDLINE 98145455
 PUBMED 9484461
 REFERENCE 2 (bases 1 to 1284)
 AUTHORS He, X.Z., Reddy, J.T., Guo, J.Z. and Dixon, R.A.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-1997) Plant Biology Division, The Samuel Roberts Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401, USA
 FEATURES Location/Qualifiers

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Best Local Similarity 76.1%; Pred. No. 1.le-136;
Matches 842; Conservative 0; Mismatches 250; Indels 15; Gaps 3;

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DEFINITION Sequence 1 from Patent WO0071736.
ACCESSION AX050436
VERSION AX050436.1 GI:12226643
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SOURCE Medicago sativa
ORGANISM Medicago sativa
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1
AUTHORS Dixon,R.A. and He,X.Z.
TITLE Isoflavonoid methylation enzyme
JOURNAL Patent: WO 0071736-A 1 30-NOV-2000;
The Samuel Roberts Noble Foundation, Inc. (US)
FEATURES
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ORIGIN

Query Match 55.6%; Score 645.4; DB 6; Length 1231;
Best Local Similarity 76.0%; Pred. No. 2.6e-136;
Matches 841; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

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Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401, USA

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Query Match 55.4% ; Score 642.2; DB 8; Length 1227;
Best Local Similarity 75.8% ; Pred. No. 1.4e-135;
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RESULT 8
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LOCUS Pisum sativum 6a-hydroxymaackiaian methyltransferase (hmm6) mRNA,
complete cds.
ACCESSION U69554
VERSION U69554.1 GI:1568636
KEYWORDS Pisum sativum (pea)
SOURCE Pisum sativum
ORGANISM Pisum sativum
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
REFERENCE 1 (Bases 1 to 1337)
AUTHORS Wu,Q., Preisig,C.L. and VanEtten,H.D.
TITLE Isolation of the cDNAs encoding (+)6a-hydroxymaackiaian
3-O-methyltransferase, the terminal step for the synthesis of the
phytoalexin pisatin in Pisum sativum
JOURNAL Plant Mol. Biol. 35 (5), 551-560 (1997)
MEDLINE 98009990
PUBMED 9349277
REFERENCE 2 (Bases 1 to 1337)
AUTHORS Wu,Q., Preisig,C.L. and VanEtten,H.D.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1996) Plant Pathology, University of Arizona,
Forbes Building, Room 204, Tucson, AZ 85721, USA
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Matches 627; Conservative 0; Mismatches 424; Indels 21; Gaps 3;

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DEFINITION ordered pieces.
ACCESSION AC136140
VERSION AC136140.8 GI:31455653
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.

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SOURCE
ORGANISM
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
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Shauli, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.
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Unpublished
2 (bases 1 to 111587)
Shauli, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.
Direct Submission
Submitted (29-OCT-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 111587)
Shauli, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Kim, D. and Roe, B.A.
Direct Submission
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OK 73019, USA
On Jun 7, 2003 this sequence version replaced gi:30061413.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 9681: contig of 9681 bp in length
* 9682 9781: gap of unknown length
* 9782 46738: contig of 36957 bp in length
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* 46839 111587: contig of 64749 bp in length.
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* /organism="Medicago truncatula"
* /mol_type="genomic DNA"
* /db_xref="taxon:3880"
* /clone="mth2-11a20"
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* /note="This is one of two clones in the same well from
* mth2-11a20"
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Best Local Similarity 58.8%; Pred. No. 2.7e-62;
Matches 699; Conservative 0; Mismatches 347; Indels 142; Gaps 3;
QY 27 ACAATGGCGGTAAGCAAGTGAAGATTTTCAAGGTCAAGCTCTCTTGTACAAACATTTGC 86
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DB 104546 TTAGTTTCTTGACCCGCTGTGATCAAGTGGGCTGTGAACTTGGCATACCATATATA 104487
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DB 104486 T-----TCAAAATCATGCAAAACCTTATTACTTCTCCGAGCTTGCTCGGCTCTTCGAA 104433

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QY 627 TCACAGCAAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAATGCAATGCTGTGGTGGAAACGTC 686
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RESULT 10
AB091686
LOCUS
DEFINITION Lotus japonicus HI4'OMT mRNA for S-adenosyl-L-methionine:
AB091686
1363 bp mRNA linear PLN 04-MAR-2003

2,7,4'-trihydroxyisoflavanone 4'-O-methyltransferase, complete cds.

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ACCESSION      AB091686
VERSION        AB091686.1 GI:28804595
KEYWORDS
SOURCE
ORGANISM       Lotus japonicus
               Lotus japonicus
               Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
               Lotus.
REFERENCE      1
AUTHORS       Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE         Generation of 7137 non-redundant expressed sequence tags from a
              legume, Lotus japonicus
JOURNAL       DNA Res. 7 (2), 127-130 (2000)
MEDLINE      20277479
PUBMED      10819328
REFERENCE      2
AUTHORS       Akashi, T., Sawada, Y., Shimada, N., Sakurai, N., Aoki, T. and Ayabe, S.
TITLE         cDNA cloning and biochemical characterization of
              s-adenosyl-L-methionine: 2,7,4'-trihydroxyisoflavanone
              4'-O-methyltransferase, a critical enzyme of the legume
              isoflavonoid phytoalexin pathway
JOURNAL       Plant Cell Physiol. 44 (2), 103-112 (2003)
MEDLINE      22497945
PUBMED      12610212
REFERENCE      3 (bases 1 to 1363)
AUTHORS       Akashi, T., Aoki, T. and Ayabe, S.
TITLE         Direct Submission
JOURNAL       Submitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University,
              Department of Applied Biological Sciences; Kameino 1866, Fujisawa,
              Kanagawa 252-8510, Japan (E-mail: ayabe@brs.nihon-u.ac.jp,
              Tel: 81-466-84-3703, Fax: 81-466-80-1141)
              Location/Qualifiers
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    Query Match 27.4%; Score 318; DB 8; Length 1363;
    Best Local Similarity 58.4%; Pred. No. 7.2e-62;
    Matches 649; Conservative 0; Mismatches 430; Indels 33; Gaps 4;
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    DB 54 ATGGAATTCAGCTCCAGCAATGGCAGTGAAGACACTGAACCTTCCCAAGCTCAGATTCAC 113
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RESULT 11
PAU82011

RESULT 12	AF502434	1253 bp	linear	PLN 14-AUG-2002
LOCUS	AF502434			
DEFINITION	Rosa hybrid cultivar orcinol O-methyltransferase (OOMT2) mRNA, complete cds.			
ACCESSION	AF502434			
VERSION	AF502434.1	GI:20514368		
KEYWORDS				
SOURCE	Rosa hybrid cultivar			
ORGANISM	Rosa hybrid cultivar			
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa. 1 (bases 1 to 1253)			
AUTHORS	Lavid, N., Wang, J., Shalit, M., Guterman, I., Bar, E., Beuerle, T., Menda, N., Shafir, S., Zamir, D., Adam, Z., Vainstein, A., Weiss, D., Pichersky, E. and Lewinsohn, E.			
TITLE	O-methyltransferases involved in the biosynthesis of volatile phenolic derivatives in rose petals			
JOURNAL	Plant Physiol. 129 (4), 1899-1907 (2002)			
MEDLINE	22167322			
PUBMED	12177504			
REFERENCE	2 (bases 1 to 1253)			
AUTHORS	Lavid, N., Wang, J., Shalit, M., Guterman, I., Bar, E., Beuerle, T., Menda, N., Shafir, S., Zamir, D., Adam, Z., Vainstein, A., Weiss, D., Pichersky, E. and Lewinsohn, E.			

TITLE Direct Submission
JOURNAL Submitted (15-Apr-2002) Vegetables Crops, Newe Ya'ar Research Center, Agricultural Research Organization, P.O. Box 1021, Ramat Yishay 30955, Israel

FEATURES
source Location/Qualifiers
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BASE COUNT 389 a 270 c 265 g 329 t

ORIGIN
Query Match 26.1%; Score 302.8; DB 8; Length 1253;
Best Local Similarity 57.3%; Pred. No. 2.1e-58;
Matches 613; Conservative 0; Mismatches 442; Indels 15; Gaps 3;

QY 29 AATGGCCGTAAAGCAAGTGAAGATTTTCAAGCTCAAGCTCTCTGTACAAACATTTGGCTT 88
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QY 89 GGCCTCATAGATCTTAAGTGTCTAAATGGATGGTTGAGCTTGACATACCGACATAATC 148
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DB |||||
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QY 704 CTCCACATGTGGTGGCTGACCTGCAAGGAAGTAAGAACTTGAATATATCTGAGGAGT 763
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QY 743 ATGTTTAAATGCATCCCAAGGCTGATGCTCTTCTGTTAAGTTGGTTTACATAATTGG 802
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RESULT 13
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LOCUS Rosa chinensis mRNA for orcinol O-methyltransferase (oomt2 gene).
DEFINITION AJ439742
ACCESSION AJ439742
VERSION AJ439742.1 GI:27527923
KEYWORDS oomt2 gene; orcinol O-methyltransferase.
SOURCE Rosa chinensis
ORGANISM Rosa chinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 1265)
AUTHORS Cock,J.Mark., Scalliet,G. and Huguenev,P.
TITLE Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1265)
AUTHORS Cock,J.Mark.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) RDP, ENSL, 46, allée d'Italie, Lyon cedex 07 69364, France
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BASE COUNT      400 a 273 c 265 g 327 t
ORIGIN
Query Match      26.1%; Score 302.8; DB 8; Length 1265;
Best Local Similarity 57.3%; Pred. No. 2.1e-58;
Matches 613; Conservative 0; Mismatches 442; Indels 15; Gaps 3;

Qy 29 AATGGCCGTAAGCAAGTGAGATTTTTC AAGTCAAGCTCTCTGTACAACATTCGCTT 88
Db 65 AATGGAGAGCATTC AAGAGCTACTTCATGCTCAAGCCACATCTCGAACCACATCTTC 124
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DB	116	AGCTTCATAAACTCCATGCTCCCTCAAATCTGCAATTC	CAATCACTAGGTATACAGATATCATC	175
QY	149	CACAGCCATGACCATGCGCCACCCATCTACTTTTTC	CAGAGTTGGTGTCAATTCACAAGTC	208
DB	176	AACAAA-----CAIGGTTACCCCATGACTCTTTCT	GAGCTCACATCTGCACCTACCAATC	229
QY	209	CCACCAACTAAAACCTGCTCAGGTGCAGAGCCCTCATGCGTTATCT	AGCACACAATGGATTC	268
DB	230	CATCCAAACCAATCCACAGAGCTCTACCGCTCATGCGCTCATGCGAATTTGGTGC	ACTCTGGCTTC	285
QY	269	TTTGAGATAGTAAGAAATCCATGACA--ACATAGAACATATGCTCTC	ACTGCTGCTTCA	325
DB	290	TTTGCTAAGAAAAAGCTGAGTAAACATGATGAGGAAGTTATACCTCT	ACTGATGATCTCC	349
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QY	386	CCAAATTTGCAAGTGCATGGAACCGAGTTGAAGAGGTGGGTTTCATGAGGAAGATCTCACA	445	
DB	410	CTGTGTTTGACCAATCCATGAGAAATCTCTGAGCACTTGGTTC	CAAAACGATGACCTACG	469
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QY	506	AACAAGTCAATCAATGAGGCATAGGCTTGTGATTTCTCAGATGTT--GAACTGGCGGTTT	562	
DB	530	GCCCATTTGATTAACAGATGCCATGGCTAGCGATGCTCGTGGTGCCTAGTGTGATCATC	589	
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DB	590	AATGATTGCAAAAGAGTGTTTGAGGATTAGAGTCATTTGGTTCGATTTGAGAGTGGTATCA	649	
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DB	650	GGAACTCTGGCAAGGCCATTTGCTGATGTCATTTCCACATATTTGAATGCATGTACTTGAT	709	
QY	683	CGTCCAAATCTGTGGAAATTTTGTCAAGGAAGCAACAAATTTGACATTTTGTGGTGGGAC	742	
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DB	770	ATGTTTGAGGCAGTTCTCTCTCCCGCATACAGTTTACTCAAGTGGATATTTGCATGACTGG	829	
QY	803	AATGACAAACATTTGCATGAGATATTTAGAAAATTTGTAAAGAGCTATTTTCAAGTGAAGC	862	
DB	830	AGCGATGAAGAAATGATCAAAATATCTTTGAGCGATCTAGAGTGGCAATTTACAGGCACAGG	889	
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QY	983	AGAAAAAGAAAGATTTGGAAGAACTCTTTCATGGAACAGGGTTTCCAAAGCTTACAAATA	1042	
DB	1010	AGGAATGAGAAAGAAATGGGTAAAGCTCTTCACTGATCTGGTTTGTAGTACTATAAGATA	1069	

QY 1043 TCTCCCTTCACAGATATTTGTCTCTATTGAGATCTATCCTTTGAATACT 1092
 |||||
 DB 1070 ACTCCCATTTCCGGGTTTAAGGTCTCTCATTTGAGGTTTATCCTTGATAATT 1119
 |||||

RESULT 15
 RCH439741 1275 bp mRNA linear PLN 06-JAN-2003
 LOCUS
 DEFINITION
 ROSA chinensis mRNA for orcinol O-methyltransferase (comt1 gene).
 ACCESSION
 AJ439741
 VERSION
 AJ439741.1 GI:27527921
 KEYWORDS
 comt1 gene; orcinol O-methyltransferase.
 SOURCE
 ROSA chinensis
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eutrosids I; Rosales; Rosaceae; Rosoideae; Rosa.
 REFERENCE
 1 (bases 1 to 1275)
 Cock,J.Mark., Scalliet,G. and Huguency,P.
 Characterisation of a novel O-methyltransferase involved in the
 biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene,
 two major scent components of rose flowers
 Unpublished
 2 (bases 1 to 1275)
 Cock,J.Mark.
 Direct Submission
 TITLE
 Submitted (25-MAR-2002) RDP, ENSL, 46, allée d'Italie, Lyon cedex
 JOURNAL
 07 69364, France
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 BASE COUNT 402 a 273 c 266 g 334 t
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 Query Match 26.1%; Score 302.4; DB 8; Length 1275;
 Best Local Similarity 57.3%; Pred. No. 2.5e-58;
 Matches 61; Conservative 0; Mismatches 446; Indels 12; Gaps 3;
 QY 29 AATGGCGGTAAACAAGTGAGATTTTTCGAAGGTCAAGCTCTCTTGTACAAACATTGGCTT 88
 DB 65 AATGGAGAGATCTCCACAGAGTACTTCTATGCTCAAGCCCACTGTGGAACCATCTTC 124
 QY 89 GGGTTCATAGATCTTAAGTGTCTTAAATGGATGGTTGAGCTTGACATACCCGACATAATC 148
 DB 125 AGCTTCATAAATCCCATGTCTCCCTCAAATCTGCAATTCAACTAGGTATACCAGATATCATC 184
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 DB 185 AACAAA-----CATGGTTACCCCATGACTCTTCTTGAGCTCACATCTGCATACCAATC 238
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|||||
299 TTTGCTAAGAAAAGCTGAGTAAACTGATGAGGAAGTTATACCTTACTGATGCTTCC 358
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743 ATGTTTAAATGCAATCCCAAGGCTGATGACAGTTCCTGCTTAAGTTGGTTTACATAATGG 802
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QY
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Db
899 AAGAAGGCAAGGTGATATCATAGATGATGATGAGAACCAAGAAAGGCGATGAGGAA 958
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983 AGAAAAGAAAGATTTGGAAGAACTCTTTCATGGAAGCAGGTTCCAAAGCTACAAATA 1042
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Job time : 4628 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 23:29:44 ; Search time 428 Seconds
(without alignments)
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Title: US-09-868-547-3

Perfect score: 1160

Sequence: 1 gttgtattatggtctt.....ataaaagtatcttgggt 1160

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1160	100.0	1160	21	AA29322 Glycine max isofla
2	645.4	55.6	1231	22	AAC89152 Alfalfa isoflavone
3	508.6	43.8	1253	21	AA29324 Glycine max isofla
4	507.2	43.7	1065	21	AA29323 Glycine max isofla
5	507.2	43.7	1065	21	AA29325 Glycine max isofla
6	497.8	42.9	1053	21	AA29321 Glycine max isofla
7	209.2	18.0	1041	20	AA290136 Coptis japonica no
8	178.4	15.4	1050	20	AA289255 (S)-3'-hydroxy-N-m

9	158.2	13.6	256	25	ABX31899 Human GDP-mannose
10	142.8	12.3	266	25	ABX23518 Human GDP-mannose
11	142.2	12.3	381	25	ABX19867 Human GDP-mannose
12	120.2	10.4	1412	20	AA25200 Maize caffeic O-me
13	118	10.2	1098	22	AA219546 Medicago sativa ca
14	118	10.2	1341	15	AAQ77692 Alfalfa COMT clone
15	114	9.8	1267	21	AA240707 Arabidopsis thalia
16	114	9.8	1314	24	AA227047 Soybean caffeic ac
17	112.4	9.7	1306	21	AAC49059 Arabidopsis thalia
18	112.4	9.7	1308	21	AAC40838 Arabidopsis thalia
19	111.8	9.6	377	25	ABX21443 Human GDP-mannose
20	111.6	9.6	1315	20	AA25201 Maize caffeic O-me
21	109.8	9.5	1368	14	AAQ38448 pPLC4 coding sequ
22	109.8	9.5	1501	24	ABK48067 cDNA encoding 5-hy
23	109.8	9.5	1503	20	AA226295 Aspen bispecific O
24	109	9.4	279	25	ABX28528 Human GDP-mannose
25	109	9.4	1507	24	ABX54111 Tobacco caffeic ac
26	108	9.3	1244	14	AAQ38449 POMT1.A and POMT1
27	108	9.3	1460	20	AA235662 DNA encoding a tob
28	107.8	9.3	1370	24	AA227040 Soybean caffeic ac
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32	106.8	9.2	1306	20	AA25202 Maize caffeic O-me
33	106.2	9.2	978	21	AAC42978 Arabidopsis thalia
34	100.2	8.6	1149	24	AB214777 Arabidopsis thalia
35	100.2	8.6	1283	21	AAC46334 Arabidopsis thalia
36	99.4	8.6	1286	21	AAC41985 Arabidopsis thalia
37	95.4	8.2	1195	24	AA227044 Soybean caffeic ac
38	94.6	8.2	1380	20	AA281875 DNA encoding a bif
39	94.6	8.2	1380	21	AAA86683 Sweetgum bifunctio
40	94.6	8.2	1380	22	AA21127 L. styraciflua ang
41	92.6	8.0	1630	21	AA468014 Eucalyptus grandis
42	90.8	7.8	1486	19	AA271042 cDNA encoding (iso
43	90.8	7.8	1486	25	AA471042 cDNA encoding (iso
44	89.6	7.7	381	21	AAA68081 Clarkia breweri IE
45	88.8	7.7	1201	21	AA288734 Eucalyptus grandis
					P. sylvestris PMT

ALIGNMENTS

RESULT 1
AAA29322
ID AAA29322 standard; cDNA; 1160 BP.
XX
AC AAA29322;
DT 26-SEP-2000 (first entry)
XX
DE Glycine max isoflavone O-methyltransferase clone srl.pk0015.b4.
XX
KW Isoflavone O-methyltransferase; soybean; degradation; daidzein;
KW Flavanoid; flower colour; growth; pollination; irradiation; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 11..1087
FT /*tag= a
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XX
PN WO200037656-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-US30338.
XX
PR 21-DEC-1998; 98US-0113190.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Famodu OO, McGonigle B, Odell JT, Fader GM, Falco SC;

XX WPI; 2000-442680/38.
 DR P-PSDB; AY9584.
 XX
 PT New polynucleotide encoding flavonoid biosynthetic enzymes for creating
 transgenic plants and for immunological screening of cDNA libraries
 XX
 PS Claim 2; Page 32; 39pp; English.
 XX
 CC AA29321-25 encode isoflavone O-methyltransferases isolated from various
 soybean (Glycine max) tissues. cDNA libraries se4, srl, srlc and sllc
 were prepared from soybean embryo (19 days after flowering), root, 8-day
 old root and seed (25 days after flowering).
 CC Isoflavone O-methyltransferase catalyses the first step in degradation
 of daidzein. Suppression of this enzyme will yield higher concentrations
 of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
 co-pigments in flower colour, stimulate pollen tube growth, attract
 pollinators, act as feeding deterrents and protect against UV
 irradiation in fruits and seeds. The cDNA and proteins can be used to
 CC isolate homologues, for immunological screening and for positive
 CC selection methods.
 XX
 SQ Sequence 1160 BP; 361 A; 197 C; 254 G; 348 T; 0 other;
 Query Match 100.0%; Score 1160; DB 21; Length 1160;
 Best Local Similarity 100.0%; Pred. No. 3.4e-295;
 Matches 1160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GTTGTCTATTAGGCTTCTTCAATTAACAAGTGGCGTAAAGCAAGTGAGATTTTCAAGG 60
 Qy 61 TCAAGCTCTCTGTACAAACATTTGCTGGTTCATAGATCTTAAGTCTTAATAATGGAT 120
 Db 61 TCAAGCTCTCTGTACAAACATTTGCTGGTTCATAGATCTTAAGTCTTAATAATGGAT 120
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 Qy 301 AGCATATGCTCTCACTGCTGCTTCAGAGTTACTTGTCAAAGCAGTGAAGTTAGT 360
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 Db 361 TCCATGTTGAGTATTTCTTGAACCAATTTCAAGTGCATGGAACCAAGTTGAAGAG 420
 Qy 421 GTGGGTTTCATGAGGAAGATCTCACAGTATTTGAGTCTCCCTTAGAACACCTTTCTGGGA 480
 Db 421 GTGGGTTTCATGAGGAAGATCTCACAGTATTTGAGTCTCCCTTAGAACACCTTTCTGGGA 480
 Qy 481 CTTTATCAATAAGACCTGCATATAACAAGTCATTCATGAGGCAATGGCTTGTGATTC 540
 Db 481 CTTTATCAATAAGACCTGCATATAACAAGTCATTCATGAGGCAATGGCTTGTGATTC 540
 Qy 541 TCAGATGTTGAACCTGGGTTTAGAGATTTGAATGGTCTTTGAGGCACTGGAATCCAT 600
 Db 541 TCAGATGTTGAACCTGGGTTTAGAGATTTGAATGGTCTTTGAGGCACTGGAATCCAT 600
 Qy 601 TGTGGATGTTGGTGGTGAAGTGAATCACAGCAAGATTTATCTGTGAGGCTTTTCTCAA 660
 Db 601 TGTGGATGTTGGTGGTGAAGTGAATCACAGCAAGATTTATCTGTGAGGCTTTTCTCAA 660
 Qy 661 GCTGAAATGCAATGTTGTTGGAAACGTCCTCAATGTTTGTGGAAATTTGTGAGGAACAA 720

Db 661 GCTGAAATGCAATGTTGTTGGAAACGTCCTCAATGTTTGTGGAAATTTGTGAGGAACAA 720
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 Qy 781 TAAGTGGTTTTACATAATTGGAATGCAACGATTTGATGATGAAGATATTAGAAAAATTGTA 840
 Db 781 TAAGTGGTTTTACATAATTGGAATGCAACGATTTGATGATGAAGATATTAGAAAAATTGTA 840
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 Db 841 AGAAGCTATTTCAGTCAAGCAAAACAGGAAGATAGTTCATAGATCTGTGATAAA 900
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 Qy 1021 AGGTTCCAAAGCTACAAAATATCTCCCTTCACAGGATATTGTCTCTTATTTGAGATCTA 1080
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 Qy 1081 TCCTTGAATACTGACGCTGCAATATTCATTTAGTAGTAAATTTGATGATTTATCAATAAA 1140
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 Qy 1141 ATAAAGTTATCTTTGTGTT 1160
 Db 1141 ATAAAGTTATCTTTGTGTT 1160

RESULT 2
 AAC89152
 ID AAC89152 standard; cDNA; 1231 BP.
 XX
 AC AAC89152;
 XX
 DT 07-MAR-2001 (first entry)
 XX
 DE Alfalfa isoflavone 4'-O-methyl transferase 8 coding sequence.
 XX
 KW Alfalfa; isoflavone 4'-O-methyl transferase 8; IOMT; transgenic plant;
 KW disease resistance; ss.
 XX
 OS Medicago sativa.
 XX
 FN W0200071736-Al.
 XX
 PD 30-NOV-2000.
 XX
 PF 15-MAY-2000; 2000WO-US13389.
 XX
 PR 20-MAY-1999; 99US-0135026.
 XX
 PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
 XX
 PI Dixon RA, He XZ;
 XX
 DR WPI; 2001-061355/07.
 XX
 PT Genetically manipulating biologically active 4'-O-methylated
 PT isoflavonoid for producing plants with increased disease resistance,
 PT and for accumulation of 4'-O-methylated isoflavonoid nutraceuticals in
 PT plants -
 XX
 PS Claim 5; Fig 2; 49pp; English.
 XX
 CC The present sequence is isoflavone 4'-O-methyl transferase 8 (IOMT)

CC coding sequence from Alfalfa. The present invention relates to a method
CC for genetically manipulating the level of biologically active IOMT. The
CC method involves transforming the target plant with a DNA fragment (the
CC present sequence) to form a transgenic plant. IOMT is useful as
CC foodstuff, nutritional supplement, animal feed supplement, nutraceutical
CC and as a pharmaceutical. Transgenic expression of IOMT in legumes is
CC useful for engineering both phytoalexin levels for improved disease
CC resistance, and health promoting nutraceutical phytochemicals. IOMT is
CC useful for engineering isoflavone 4'-O-methylation, or other organisms
CC that do not naturally produce isoflavonoids.

XX SQ Sequence 1231 BP; 402 A; 183 C; 235 G; 411 T; 0 other;

Query Match 55.6%; Score 645.4; DB 22; Length 1231;
Best Local Similarity 76.0%; Pred. No. 9.7e-160;
Matches 841; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

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DB 29 CTTTCATCAATTAATGGCGGAAACCAAGTGAAATTTTCAAGCAACAAGCTTTATTATACA 88
QY 78 AACATTTCCTGGCTTCATAGATTCTAAGTGTCTAAATGATGGTTGAGCTTGACATAC 137
DB 89 AACATATATATGCTTCATAGATTCCATGCTCTTAATGGCTGTGTAATGAACATAC 148
QY 138 CCGACATAATCCACAGCATAGCCATGCCAACCCATTACTTTTTCAGAGTTGGTGTCAA 197
DB 149 CAAACATAAT-----CCAAACCATGGCAACCAATTTCTCTTCAAACTTAGTTCAA 202
QY 198 TTCTACAGTCCCNCAACTAAACTCGTCAGGTGCGAGAGCTCATGCTGTATCTACAC 257
DB 203 TTCTTCAAGTCCATCGTCGAAATAGGTAACTGCGGGCTCTCATGCTTACCTCGCG 262
QY 258 ACAATGATTCTTTGAGATAGTAGAATCCATGACACATAGAGCATATGCTCTCACTG 317
DB 263 ACACGGATTCTTCGAGATATACAAAGAGA-----AGAGTCTTATGCTCTCACTG 316
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DB 317 TTGCTTCAGAGCTCTTTGTTAGAGCGAGTGATCTTTGTTAGCCCAATGGTTGAGTGTG 376
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DB 437 ATCTTACACTTTTGGTGTACTTTAGAGTCTGTTTTGGGATTTTCTTGATNAAAATC 496
QY 498 CTGCATATAACAGTCAATCAATGAGGCAATGGCTTGATTTCTCAGATGTTGAACCTGG 557
DB 497 CTGAATATAATACCTCATTTAATGATGCAATGGCTAGTATTTCAAATTTGATAAATGG 556
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QY 618 GAACCTGAATCACAGCAAGATTATCTGTAGGCTTTTCTPAAGCTGAAATGCAATGCTGT 677
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DB 917 ATCAAGTTACTCAATTAAGCTCTCTTATGATGTAAACATGGCTTG---TCTAAATGAA 973
QY 978 AAGAGAGAAAGAGAGATTTGAAGAAACTTTCATGGAGCAGGCTTCCAAAGCTACA 1037
DB 974 AAGAGAAATGAGGAGAAATGGAAGAACTTTCATAGAGCTGGTTTCCAACTATA 1033
QY 1038 AATATCTCTCCATCAGAGATATTCTCTTATGAGATCTATCTTGAATCTGACGC 1097
DB 1034 AGATATCTCTTGAAGTGGATTTTGTCTTATGAGATCTATCCATAAAGCTTTTGC 1093
QY 1098 TGCATATTCATTTAGTGTAAATT 1124
DB 1094 TTTGATCATTCATCCATTTCTATTGTTT 1120
RESULT 3
AA29324
ID AAA29324 standard; cDNA; 1253 BP.
XX AAA29324;
XX AC AC
XX XX
DT 26-SEP-2000 (first entry)
XX
DE Glycine max isoflavone O-methyltransferase clone sslc.pk002.di.
XX
XX Isoflavone O-methyltransferase; soybean; degradation; daidzein;
XX Flavanoid; flower colour; growth; pollination; irradiation; ss.
XX
XX Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 2..1048
FT /tag= a
FT /product= Isoflavone_O-Methyltransferase
FT /partial
XX WO200037656-A2.
XX
XX 29-JUN-2000.
XX
XX 20-DEC-1999; 99WO-US030338.
XX
XX 21-DEC-1998; 98US-0113190.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Ramodu CO, McGonigle B, Odell JT, Pader GM, Falco SC;
XX
XX WPI; 2000-442680/38.
XX P-PSDB; AAY96586.
XX
XX New polynucleotide encoding flavonoid biosynthetic enzymes for creating
XX transgenic plants and for immunological screening of cDNA libraries
XX
XX Claim 2; Page 35; 39pp; English.
XX
XX AAA29321-25 encode isoflavone O-methyltransferases isolated from various
XX soybean (Glycine max) tissues. cDNA libraries s4, s1, srlc and sslc
XX were prepared from soybean embryo (19 days after flowering), root, 8-day
XX old root and seed (25 days after flowering).
XX Isoflavone O-methyltransferase catalyses the first step in degradation
XX of daidzein. Suppression of this enzyme will yield higher concentrations
XX of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
XX co-pigments in flower colour, stimulate pollen tube growth, attract
XX pollinators, act as feeding deterrents and protect against UV
XX irradiation in fruits and seeds. The cDNA and proteins can be used to
XX isolate homologues, for immunological screening and for positive

CC selection methods.

XX Sequence 1253 BP; 374 A; 232 C; 267 G; 380 T; 0 other;
SQ Query Match 43.8%; Score 508.6; DB 21; Length 1253;
Best Local Similarity 68.2%; Pred. No. 1e-123;
Matches 754; Conservative 0; Mismatches 339; Indels 12; Gaps 3;

QY 34 CCGTAAAGCAAGTGAAGATTTTCAAGTCAAGCTCTCTGTGACAAAATTTGGCTT 93
Db 1 CCAAAAAGCAATGGAATCTTTGAGGCCAATCTCTTTGTACATGAGCTATATGGCA 60

QY 94 CATAGATTTAAAGTGTCTAAATGGATGGTTGACCTTGACATACCCGACATAATCCACAG 153
Db 61 CCTAAGACCTATGTCTTAAAGTGGCTGTTCACTAGGTATTTCCACATATAT----- 114

QY 154 CCATAGCATGGCCAAACCATTAATTTTTCAGATTTGGTGTCAATTTCAAGTCCCAAC 213
Db 115 ACAGAACCATGCCAAACCCATTAATCTTTCTGATTTGGTCTCTACTCTTCAATTTCCACC 174

QY 214 AACTTAAACTCGTCAGTGGAGCCCTCATGCTTATCTAGCACACATGGATCTTTGA 273
Db 175 ATCTAAGCTGGTTTGTGACAGTTCATGCGCTTTTGGCACACATGGAATCTTTGA 234

QY 274 GAT---AGTAAGATCCATGACAAACATAGACATATGCTCTCACTGCTCTCAGAGTT 330
Db 235 TATCCGTGAGACCAAGATGATCATGAATTAGCATATGCTCTAACCCCTGCTTCAAGCT 294

QY 331 ACTTGTCAAAGCAGTGAAGTATTTAGTCTCAATGCTTGAATTTTCTTGAACCAAA 390
Db 295 TCTAGTTAGTTCAGTGAACCACTCTTTATCTCCAAATGCTTCGATGAATCTGATCCACT 354

QY 391 TTGTCAAGTGCATGGAACAGTGAAGAGTGGTTCATGAGGAAGATCTCACAGTATT 450
Db 355 TCTGATGACTACATACCATCTTTGGGAATGATTCGTTGGGAAGACCCACAGTACA 414

QY 451 TGAGGCTCTCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCTGATATAACAA 510
Db 415 TGACAGAGCTTTGGAAACAGCTTTTGGGACTCTTTGAGAAAACCTTACACAAATGAG 474

QY 511 GTCAATTCAGTGAAGCAATGGCTTGTGATCTCAGATGTTGAATGTTGGCGTTAGAGATT 570
Db 475 TCTCTTCAATGAGCTATGGCAAGTGAATCCCGAATGGTAGCTTGGCACTCAAAAATTG 534

QY 571 CAATTGGTCTTTGAGGAGCTGGATCCATGTCATGTTGGTGGTGAAGTGAATCAC 630
Db 535 CACTTCAGTTTGAAGGGCTAGATTCATGTTGGATGTTGGTGGTGAAGTGAAGCCAC 594

QY 631 AGCAAGATTATCTGTGAGGCTTTTCTTAAGCTGAAATGCATGTTGTGAACGCTCCAAA 690
Db 595 AGCCAGAAATATCTGTGAGGCTTTCCGAAGTTCGAATGTGTTGCTTGACCTTCTCA 654

QY 691 TGTGTGGAAATTTGTCAGGAACCAATTTGACATTTGTTGGTGGGACATGTTTAA 750
Db 655 TGTGTGAGAAACTTTCAGAGAACCAATAATTTGAGTTTGTGGTGGTGAAGTGTCAA 714

QY 751 ATGCATCCCAAGGCTGATGAGTTCCTTAACTGCTTTTACATATTTGGAATGACAA 810
Db 715 CTCTTTCCTCAACTGATGAGTTCCTTAAAGTGGTTTACATATTTGGAATGACGA 774

QY 811 CGATTGATGAAGATTTAGAAAATTTGAAGAGCTATTTCAGGTGAAAGCAAAACAGG 870
Db 775 AAATGTCATAAAGATCTGMAAAAGTGTAAAGATCTTATTTCAGCAAGCAAGCACAGG 834

QY 871 AAAGTATGTCATAGATCTGTGATAACGAAACAAAGATGAGCGCCAGTCTCTGA 930
Db 835 AAAAGTGATTATCATAGATATAATAAATGAGAGCTAGATGACCCGGATGACTCG 894

QY 931 ACTAAAGCTCTTCTGATGATGACATGCGGATGATTTATTAATGGAAGAGGAAAGA 990
Db 895 AACAAAGCTTAGTTTGGATATAGTTATG---TCGACTATGATGGAAGAGGGAAGTGA 951

QY 991 AGAAGATTGGAAGAACTCTTTTCATGGAAGCAGGCTTCCAAAGCTTACAAAATATCTCCCTT 1050

Db 952 AAAAGAATGGAACAAATGTTCAATTTGAGCGGATTCCAACACTGCAAAATATTTCCCAT 1011
QY 1051 CACAGGATATTTGCTCTCTTATTGAGATCTATCTTGAATACTGACGCTGCAATATTCAT 1110
Db 1012 CTTTGGTTTCAGATCTCTAATTTGAGCTCTATCTTTAGACATATATCTAGCTTGTATGC 1071

QY 1111 TTAGTAGTTAAATTTGATGTTATCA 1135
Db 1072 ATTTATAGTTTGGCATGTTGTGA 1096

RESULT 4
AA29323
ID AAA29323 standard; cDNA; 1065 BP.
XX
AC AAA29323;
XX AC
DT 26-SEP-2000 (first entry)
XX
DE Glycine max isoflavone O-methyltransferase clone srlc.pk001.b16.
XX Isoflavone O-methyltransferase; soybean; degradation; daidzein;
KW Flavonoid; flower colour; growth; pollination; irradiation; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 1..1065
FT FT /*tag= a
FT FT /transl_except= (pos:268..279, aa:Glu)
FT FT /note= "A 9 bp insertion is present"
XX
PN WO200037656-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-US30338.
XX
PR 21-DEC-1998; 98US-0113190.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Ramodu OO, McConigle B, Odell JT, Fader GM, Falco SC;
XX
DR WPI; 2000-442680/38.
DR P-PSDB; AAY96585.
XX
PT New polynucleotide encoding flavonoid biosynthetic enzymes for creating
PT transgenic plants and for immunological screening of cDNA libraries
XX
PS Claim 2; Page 33-34; 39pp; English.

CC AAA29321-25 encode isoflavone O-methyltransferases isolated from various
CC soybean (Glycine max) tissues. cDNA libraries se4, srl, srlc and sllc
CC were prepared from soybean embryo (19 days after flowering), root, 8-day
CC old root and seed (25 days after flowering).
CC Isoflavone O-methyltransferase catalyses the first step in degradation
CC of daidzein. Suppression of this enzyme will yield higher concentrations
CC of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
CC co-pigments in flower colour, stimulate pollen tube growth, attract
CC pollinators, act as feeding deterrents and protect against UV
CC irradiation in fruits and seeds. The cDNA and proteins can be used to
CC isolate homologues, for immunological screening and for positive
CC selection methods.
XX
SQ Sequence 1065 BP; 315 A; 212 C; 233 G; 305 T; 0 other;

Query Match 43.7%; Score 507.2; DB 21; Length 1065;
Best Local Similarity 69.2%; Pred. No. 2.2e-123;
Matches 740; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

QY 21 CATTAACAATGCGCCGTAAAGCAAGTGAGATTTTCAAGTCAAGCTCTTCTGTCAAC 80

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Db 5 CTTCAATGAATAACCAAAAGAAATTCAGCTCTTTGAGGGCCAATCTCTCTGTACATGC 64
Qy 81 ATTGTGTTGGCTTCATAGATCTTAAGTGTCTAAATCGGTGATGAGCTTGACATACCG 140
Db 65 AGCTATATGGCGACCTTAAGACCTATGTTCTTAAGTGGGCTGTTCAACTAGGTATTCAG 124
Qy 141 ACATAATCCACAGCATAGGCGATGGCCAAAGCCCAATCTTTTCAGAGTCTGGTGTCAATTC 200
Db 125 ACATAAT-----ACAGAACCATGCCAAACCCATTTCTTCTTGACTTGGTCTCTACTC 178
Qy 201 TACAAGTCCACACCACTAAATCTCGTCAAGTGCAGAGCCCTCATGCGTTATCTAGCACACA 260
Db 179 TTCAAATTCACACAGTCAAGCTCTTTTGTGAGCGGTTTCATGCGCTTCTTGCCACACA 238
Qy 261 ATGGATTTCTTGAGATAGTAGAATCCATGACACATAGA---AGCATATGCTCTCACTG 317
Db 239 ATGNAATCTTTGAGATCCATGAGAGCCCAAGAAATCATGAATACATATGCTCTAACCC 298
Qy 318 CTGCTTCAGAGTTACTTGTCAAAAGCAGTGAAGTCTAGTTAGTCTCCCAATGGTTGAGTAT 377
Db 299 CTGCATCAGAGCTCTTGTCTAATAGTAGTATCATTTCTCTATCTCCAAATGGTTCTAGCT 358
Qy 378 TTCTTGAAACCAATTTCAAGTGCATGGAACCAAGTTGAAGAGTGGGTTTCATGAGGAAG 437
Db 359 TTACCGATCCACTTCGGAACGTTAAATACCATCACATTGGGGGAATGGAATCGTGGGAGG 418
Qy 438 ATCTCACAGTATTTGAGGTCTCTTAGGAACACACCTTTCTGGGACTTTATCAATAAAGACC 497
Db 419 ACCCTCAGTATTTGAGAGAGCCCAAGGAACAGCGTTGGGGACTTCTTGAGAAAATC 478
Qy 498 CTGCATATAACAAGTCAATCAATGAGGCAATGGCTTGTGATCTCTCAGATGTTGAACCTGG 557
Db 479 CTGAATATTTAGTCTCTTCAATGAGGCTATGCAAGTGAATCCGGAATAGTAGACTTGG 538
Qy 558 CGTTTAGAGATTCGAATGGGCTTTGAGGAGCTGGAATTCATTTGCGATGTTGGTGGTG 617
Db 539 CACTCAAAAATTTGCACTTCAGTTTCTTGGGGGCTAGATTCATGCTGGATGTTGGTGGTG 598
Qy 618 GAATGGAATCAGACCAAGATATCTGTGAGGCTTTTCTTAAGTCAAAATGCATGCTGT 677
Db 599 GAATGGAATCAGGCGCAGAAATATCTGTGACGCAATTTCTTAAGTGAATGTTGTTGTC 658
Qy 678 TGAACCTCCAAATGTTGTGAAAATTTGTGAGGAACCAATTTGACATTTGTTGGTG 737
Db 659 TTGACCTTCTCATGTTGTAGAGAACTTGACAGGACCAATATTTGAGTTTGTGGTG 718
Qy 738 GGCACATGTTTAAATGATCCCAAGGCTGATGAGTCTGCTTTAAGTTGGTTTACATA 797
Db 719 GTGACATGTTCAACTCTATCCCTCAAGCTGATGCACTACTAAAGTGGGTTTACATA 778
Qy 798 ATTGGAATGACACGATTTGCATGAAGATATTAGAAAATTTGAAAGAGCTATTTCAGGTG 857
Db 779 ATTGGCCGACGAAAATTTGATAAAGATCTTGAAAAGTGTAGAGATCTATTTCAGCA 838
Qy 858 AAAGCAAAACAGGAAAAGTAGTTGCTCATAGATCTGTGATAAAGCAAAACAAAGATGAGC 917
Db 839 AAGCAACAGTGGAAGTAGTATCATAGATGCGTAAATGAATGAGAGCTAGATGACC 898
Qy 918 GCGAAGTTACTGAACCTAAAGCTCCTTAAGGATGACACATGGCATGATTTAATGAAGAA 977
Db 899 CGGATATGACACAAACAAAGCTTAGTTTGGACATATTATG---TTGACGATGAATGAA 955
Qy 978 AAGAGAGAAAGAGAGATGGAAGAACTCTTCATGGAGCAGGCTTCCAAAGCTTACA 1037
Db 956 GAGAGAGAACGGAAGAAAGATGGAAGAACACTCTTCATCGAAGCAGGATCAACACTACA 1015
Qy 1038 AAATATCTCCCTTTCACAGGATATTGTCTCTTATTGAGATCTATCTCTGA 1087
Db 1016 AATATTTCCATCTTTGGTTTATAGATCTCTGATTTGAGGCTATCTCTTGA 1065
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RESULT 5

```
AAA29325
ID AAA29325 standard; cDNA; 1065 BP.
AC AAA29325;
XX
DT 26-SEP-2000 (first entry)
XX
DE Glycine max isoflavone O-methyltransferase clone sr1c.pk001.b16.
XX
KW Isoflavone O-methyltransferase; soybean; degradation; daidzein;
KW Flavanoid; flower colour; growth; pollination; irradiation; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 4..1065
FT /tag= a
FT /transl_except= (pos:368..279, aa:Glu)
FT /note= "A 9 bp insertion is present"
XX
PN WO200037656-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-US30338.
XX
PR 21-DEC-1998; 98US-0113190.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Famodu OO, McGenigle B, Odell JT, Fader GW, Falco SC;
XX
DR WPI; 2000-442680/38.
XX
DR P-PSDB; AAY96587.
XX
PT New polynucleotide encoding flavonoid biosynthetic enzymes for creating
XX transgenic plants and for immunological screening of cDNA libraries
XX
PS Claim 2; Page 37; 39pp; English.
XX
CC AAA29321-25 encode isoflavone O-methyltransferases isolated from various
XX soybean (Glycine max) tissues. cDNA libraries seq, srl, srlic and sslic
XX were prepared from soybean embryo (19 days after flowering), root, 8-day
XX old root and seed (25 days after flowering).
XX CC Isoflavone O-methyltransferase catalyses the first step in degradation
XX of daidzein. Suppression of this enzyme will yield higher concentrations
XX of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
XX co-pigments in flower colour, stimulate pollen tube growth, attract
XX pollinators, act as feeding deterrents and protect against UV
XX irradiation in fruits and seeds. The cDNA and proteins can be used to
XX isolate homologues, for immunological screening and for positive
XX selection methods.
XX
SQ Sequence 1065 BP; 315 A; 212 C; 233 G; 305 T; 0 other;
Query Match 43.7%; Score 507.2; DB 21; Length 1065;
Best Local Similarity 69.2%; Pred. No. 2.2e-123;
Matches 740; Conservative 0; Mismatches 318; Indels 12; Gaps 3;
Qy 21 CATTAACAATGCCCGTAAGCAAGTGAAGTCTTTCAAGGTCAAGCTCTCTTGTACAAAC 80
Db 5 CTTCAATGAATAACCAAAAGAAATTCAGCTCTTTGAGGGCCAATCTCTCTGTACATGC 64
Qy 81 ATTGTGTTGGCTTCATAGATCTTAAGTGTCTAAATCGGTGATGAGCTTGACATACCG 140
Db 65 AGCTATATGGCGACCTTAAGACCTATGTTCTTAAGTGGGCTGTTCAACTAGGTATTCAG 124
Qy 141 ACATAATCCACAGCATAGGCGATGGCCAAAGCCCAATCTTTTCAGAGTCTGGTGTCAATTC 200
Db 125 ACATAAT-----ACAGAACCATGCCAAACCCATTTCTTCTTGACTTGGTCTCTACTC 178
Qy 201 TACAAGTCCACACCACTAAATCTCGTCAAGTGCAGAGCCCTCATGCGTTATCTAGCACACA 260
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Db 179 TTCAAATCCACGCTAACGCTGCTTTTGTGACGGCTTCATGGCTCTTGTGGCACACA 238
Qy 261 ATGGAATCTTTGAGATAGTAGAATCCATGACACATAGA---AGCATATGCTCTCACTG 317
Db 239 ATGGAATCTTTGAGATCCATGAGAGCCAAAGAGATCATGAACATAACATATGCTCTAAACC 298
Qy 318 CTGCTTCAGAGTACTTCTGTCACAAAGCAGTGAAGCTTAGTTTGTAGCTCCAAATGTTGAGTATT 377
Db 299 CTGATCAAGACTTCTGTCATATAGTAGTAGTATCATATGTCATCTCCAAATGTTCTAGCGT 358
Qy 378 TTCTTGAACCAAAATTTGCAAGTGCATGGAACCAAGTTCGAAGAGGTGGGTTTCATGAGGAAG 437
Db 359 TTACCGATCCACTTCGGAACGTTAAATACCATCACTTGGGGAATGGAATCGTGGGAGG 418
Qy 438 ATCTCAGAGTATTTGAGTCTCTTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACC 497
Db 419 ACCCTCAGTATTTGAGACACGCCACCGAAACAGCGCTTGGGACTTCTTGGAGAAAATC 478
Qy 498 CTGATATTAACAAGTCAATTCATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACCTGG 557
Db 479 CTGAATATTTAGTCTCTTCAATGAGGCTATGGCAAGTATCCGATAGTAGACTTGG 538
Qy 558 CGTTTAGAGATGCAATTTGGTCTTTGAGGACGTGAATCATTTGTGATGTTGGTGTG 617
Db 539 CACTCAAAAATTTGCACTTCAGTCTTTTGGGGGCTAGATTCCATGCTGGATGTTGGTGTG 598
Qy 618 GAACTGGAATCACAGCAAGATTTATCTGTGAGGCTTTTCCCTAAGCTGAATGCAATGCT 677
Db 599 GAATGGAACACCGCCAGAAATTTCTGTGACGCAATTTCCCTAAGTTGAATTTGTGTGTC 658
Qy 678 TGGAACTGCCAAATTTGTGGAAATTTTGTGAGGACCAACAATTTGCAATTTGTTGTGTG 737
Db 659 TTGACCTTCCTCATGTTGTGAGAACTTGACAGGACCAATAATTTGAGTATTGTTGTGTG 718
Qy 738 GGGACATGTTTAAATGATCCCAAGGCTGATGAGTGTCTGCTTAAGTTGGTGTGTTACATA 797
Db 719 GTGACATGTTCAACTCTATCCCTCAAGCTGATGCACTGCTACTAAAGTGGGTTTACATA 778
Qy 798 ATTGGAATGACAACGATGTCATGAAGATATTAGAAATTTGTAAGAAGCTATTTCAAGTG 857
Db 779 ATTGGAACGCAAAATTTGCATTAAGATCTTGCAAAAGTGTAGAGATTTCTATTTCAAGCA 838
Qy 858 AAAGCAAAACAGGAAAGTAGTTGTCTATAGATPACTGTGATATAACGAAACAAAGATGAGC 917
Db 839 AAGGCAACAGTGGAAAGTAGTATATCATAGATGCGGTAAATAATGAGAAGCTAGATGACC 898
Qy 918 CCCAAGTTACTGAACATAAGCTCCTTATGGATGTACATGTCATGATGATATTTAATGGAA 977
Db 899 CGGATATGACACAAACAAGCTTAGTTTGGACATTTATTATG---TTGACGATGAATGGAA 955
Qy 978 AAGAGAGAAAAGAAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACA 1037
Db 956 GAGAGAGACGGAAGAAAGATGGAACAACTCTTCATGAGACGAGGATTCAAACNCTACA 1015
Qy 1038 AAATATCTCCCTTCACAGATATTTGTCTCTTATTGAGATCTATCCCTTGA 1087
Db 1016 AAATATTTCCCATCTTTTGGTTTGTAGATCTCTGATTGAGTCTATCCCTTGA 1065
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RESULT 6

AAA29321
ID AAA29321 standard; cDNA; 1053 BP.

XX AC AAA29321;

DT 26-SEP-2000 (first entry)

DE Glycine max isoflavone O-methyltransferase clone se4.pk0007.all.

KW Isoflavone O-methyltransferase; soybean; degradation; daidzein;

XX Flavonoid; flower colour; growth; pollination; irradiation; ss.

OS Glycine max.

```
XX FH Key Location/Qualifiers
CDS 1..1053
FT /*tag= a
FT /product= Isoflavone_O-Methyltransferase
FT /partial
XX XX WO200037656-A2.
XX XX 29-JUN-2000.
XX XX 20-DEC-1999; 99WO-US30338.
XX XX 21-DEC-1998; 98US-0113190.
XX XX (DUFO) DU PONT DE NEMOURS & CO B I.
XX XX Famodu OO, McGonigle B, Odell JT, Fader GM, Falco SC;
XX XX WPI; 2000-442680/38.
XX XX P-PSDB; AAY96583.
XX XX New polynucleotide encoding flavonoid biosynthetic enzymes for creating
transgenic plants and for immunological screening of cDNA libraries
XX XX Claim 2; Page 30; 39pp; English.
XX XX AAA29321-25 encode isoflavone O-methyltransferases isolated from various
soybean (Glycine max) tissues. cDNA libraries se4, srl, srlic and sslic
were prepared from soybean embryo (19 days after flowering), root, 8-day
old root and seed (25 days after flowering).
XX XX Isoflavone O-methyltransferase catalyses the first step in degradation
of daidzein. Suppression of this enzyme will yield higher concentrations
of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as
co-pigments in flower colour, stimulate pollen tube growth, attract
pollenators, act as feeding deterrents and protect against UV
irradiation in fruits and seeds. The cDNA and proteins can be used to
isolate homologues, for immunological screening and for positive
selection methods.
XX XX SQ Sequence 1053 BP; 323 A; 198 C; 226 G; 306 T; 0 other;
Query Match 42.9%; Score 497.8; DB 21; Length 1053;
Best Local Similarity 68.9%; Pred. No. 6.5e-121;
Matches 730; Conservative 0; Mismatches 317; Indels 12; Gaps 3;
Qy 30 ATGGCCCTTAAGCAAGTGAATTTTCAAGTCAAGCTCTCTGTGACAAATTTGCTTG 89
Db 2 ATAACCAAAAAGCAATGGAACCTCTTTGAGGGCCAATCTCTTTGTACATGCGCTATACG 61
Qy 90 GCTTCATAGATTTCTAAGTGTCTAAATGGATGGTGGCTTGACATACCCGACATAATCC 149
Db 62 GGCACCTTAAGACCTATGTGCTTAAGTGGGCTGTTCAACTAGGTATTTCGACATAAT- 119
Qy 150 ACAGCCATAGCCATGGCCAAACCCATTACTTTTTCAGAGTTGGTGTCAATTTCTACAAGTCC 209
Db 120 ----ACAGAACCATTGCCAAACCCATTACAGTTCTTGACTTGGTTTCTACTCTTCAAATTT 175
Qy 210 CACCAACTAAACTCGTCAGGTGAGAGCCCTCATGCGTTATCTTAGACACAAATGGATTCT 269
Db 176 CACCATCTAAGGCTGGTTTGTGCGAGTTCATGCGCTTTTGGCACAGGATGGAATCT 235
Qy 270 TTGAGAT---AGTAAGAATCCATGACACATAGAACATATGCTCTCACTGCTGCTTCAG 326
Db 236 TTGATATCCGTGAGAGCCAAAGATCATGAATTAGCATATGCTCTAACCCCTGCATCAA 295
Qy 327 AGTTTACTTGTCAAAAAGCAGTGAGCTTAGTTTAGTCCAAATGGTTGAGTATTTTCTTGAAC 386
Db 296 AGCTTCTAGTTAGTTGAGTGACCACTGTTTATCTCCAAATGGTTCGATGAATCTGATC 355
Qy 387 CAAATGCTCAAGTGCATGGAACCAAGTTGAAGAGGTGGTTCATGAGGAAGATCTCAAG 446
Db 356 CACTTCTGATGACTATACATACATCACTTTTGGGGAATGGATTCTGTTGGGGAAGACCCACAG 415
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Db      841 GTGACATGCTCTTAATGTGCAATCAGAACATCCTTA---TACCAGATGAGACTGACT 897
Qy      944 ATGATGTACATGGCATGTATTATTAAATGAAAGAGAGAGAAAGAAAGATTTGGAAG 1003
Db      898 TTGATTTGGACATGATGCTCAACACTGGAGGAAAGAGAGAGACTGAAGAGGATTTGGAAG 957
Qy      1004 AAACTCTTCATGGAGCAGGGTTCAAAAGCTACAAAATATCTCCCTTCACAGGATTTTG 1063
Db      958 AAGCTCATCCATGATGTCAGGGGTACAAAGGGCATAAGATAACACAAATTAAGTCTGTACAA 1017
Qy      1064 TCTCTTATTGAGATCTATCCCT 1085
Db      1018 TCTGTGATTGGCTTATCCAT 1039

RESULT 8
AAx89255
ID AAX89255 standard; cDNA; 1050 BP.
XX
AC AAX89255;
XX
DT 20-SEP-1999 (first entry)
DE (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase encoding cDNA.
KW (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase; 4'-OMT;
KW enzyme; secondary metabolite; reticuline; drug; ss.
XX
OS Coptis japonica.
XX
PN JP11178579-A.
XX
PD 06-JUL-1999.
XX
PF 24-DEC-1997; 97JP-0355320.
XX
PR 24-DEC-1997; 97JP-0355320.
XX
PA (MITC ) MITSUI PETROCHEM IND CO LTD.
XX
DR WPI; 1999-437312/37.
XX
P-PSDB; AAY27183.
XX
PT New (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase - and
XX gene encoding it
XX
PS Claim 5; Fig 12; 28pp; Japanese.
XX
CC This cDNA encodes a polypeptide having the enzymatic activity of (S)-3'-
XX -hydroxy-N-methylcoclaurine 4'-O-methyltransferase (4'-OMT). A vector
XX containing the DNA can be used to transform a microbe for the recombinant
XX preparation of the enzyme. The enzyme can be used to prepare a secondary
XX metabolite of a plant derived from reticuline which is useful as a raw
XX material for drugs.
XX
SQ Sequence 1050 BP; 313 A; 191 C; 252 G; 294 T; 0 other;

Query Match 15.4%; Score 178.4; DB 20; Length 1050;
Best Local Similarity 51.3%; Pred. No. 7.7e-37;
Matches 528; Conservative 0; Mismatches 481; Indels 21; Gaps 4;

Qy      57 AAGGTCAGAGCTCTCTTGTACAAACATTTGCTTGGCTTCATAGATCTAAGTGTCTAAAT 116
Db      38 AAGCTCAAGCTCATGTGTGAAAANTCACTATGTTTTCAGATTCCTTAGTCTCCGAT 97
Qy      117 GGATGGTTGAGTTGCACATACCAGACATAATCCAGCCATAGCCATGCCAACCCATT 176
Db      98 GTGCAGTGGAACCTTGAATCGTCGACAT-----CATGATAACACAAACCCATCCATG 151
Qy      177 CTTTTCAGAGTTGGTGCAATCTACAGTCCACCACTAACTGCTGAGGTGCGAGA 236
Db      152 CACTTGGCGATCTGGCATCTAAGCTTCTGTTTCGGATGTGAATTGCGATAATTGTATC 211

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Qy      237 GCCTCATGCGTTATCTAGACACAAATGGATCTTTTGGAGATAGTAAGAAATCCATGACAA 296
Db      212 GGATATTACGATACTTGGTGAATAATGAAATACTGAGAGTGGAAAAATCTGATGATGGT 271
Qy      297 TAGAAGCATATGCTCTCAGTCTGCTTTCAGAGTTACTTTGTCAAAAGCAGTGAGCTTAGT 356
Db      272 AGAAGAAGTACGGCTTGAACCTTATTCACACATTTGCTTCAAGGAATGCCAAGAGGAGTA 331
Qy      357 TAGCTCCAAATGGTTAGTATTTTCTTGAACCAATTTCTCAAGGTGCAATGAACCAAGTTGA 416
Db      332 TGGTTCCAAATGATTTCTTGAATGACTCAAAAAGATTTTATGACTCTCTTGGCATTCATGA 391
Qy      417 AGAGTGGGTTTCATGAGGAATCTCACAGTATTTGAGGTCTCTTATAGGAACACCTTTCT 476
Db      392 AGGATGGCTTTAAGTGCACATGGTC---ATGCTTTTGAAGAAGGCCATGGGAATGACTATAT 448
Qy      477 GGGACTTTATCAATAAAGAGCCCTGCATATAACAGTCAATCAATGAGGCAATGGCTTGTG 536
Db      449 GGGAGTACTTGGAGGACACCCCTGATCAAGGCCAATTTTCAATGAAGGCAATGSCCGGTG 508
Qy      537 ATTCTCAGATGTTGAATGCGGTTTACAGATTCGAATTCGATGGG---TCTTTGAGGAGCTGG 593
Db      509 AAACAGAGCTTCTCACTTCTTCACTCATATCTGGAAGTAGAGATATGTTCAAGGTATTG 568
Qy      594 AATCCATTGGGATTTGGTGGTGGAACTGGAATCACAGCAAGATTTATCTGTGAGGCTT 653
Db      569 ACTCATTGTTGATGTTGGTGGAGAAATGGTACTCTGTCAAGGCCATTTCTCAGCGAT 628
Qy      654 TTCCTAAGCTGAAATGCTGTTGGAACTGTCAAAATGTTGTGAAAAATTTGTCAGGAA 713
Db      629 TTCACATATCAAGTGCACCCCTCTTGTATCTCCCTCATGTCAATTCCTATGACC 688
Qy      714 GCAACAATTTGACATTTGTTGGTGGGACATGTTTAAATGCATCCCCAAGCTGATGCAG 773
Db      689 TTCCTAATATTGAACGAATTTGGTGGCGACATGTTTAAATCCGTGCCAGTCCCAAGCTA 748
Qy      774 TTCTGCTTAAGTTGGTTTACATAATTTGGAATGACACAGATTCGATGAAGATATTAGAA 833
Db      749 TCATCTCAAGCTAATTTTGCACGATTGGAATGGAAGACTCGATCAAGATTTTAAAGC 808
Qy      834 ATTGTAAGAGCTATTTTCAGGTGAAAGCAAAAACAGGAAAAGTAGTTCTCATAGATCTG 893
Db      809 AATCGAGAATTCAGTCCCA-----AAAGATGGAGGAAAGTATATAGTGGATG 859
Qy      894 TGATAACGAAAAACAAAGATGAGCGCCAAAGTACTGAACCTAAAGCTCCTTATGATGATAC 953
Db      860 TGGCATTAGATGAGGAGTCAGACCATGAGCTTAGCAGCACACGATTCCTTATATCG 919
Qy      954 ACATGGCATGTATTATTAAATGGAAGAGAGAGAGAAAAGAGATTGGAAGAAACTCTTCA 1013
Db      920 ATATGTTGGTGAACACTGGTGGTAAAGAGCGGACTAAAGAGTTTGGAGAAAATTTGTGA 979
Qy      1014 TGGAAGCAGGGTTCCAAAGCTACAAAATATCTCCCTTCACAGGATATTTGCTCTTATTG 1073
Db      980 AAAGTGCAGGATTTAGTGGTTGCAAAATCAGGCACATAGCGCTATACAAATCACTCAT 1039
Qy      1074 AGATCTATCC 1083
Db      1040 AGGTTTTTCC 1049

RESULT 9
ABX31899
ID ABX31899 standard; cDNA; 256 BP.
XX
AC ABX31899;
XX
DT 11-FEB-2003 (first entry)
XX
DE Human GDP-mannose 4,6-dehydratase (GM4, 6D) DNA #13956.
XX
KW Human; GDP-mannose 4,6-dehydratase; GM4, 6D; gene; ss; inflammation;

```

KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW complex carbohydrate; gene replacement therapy; immunosuppressive;
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW antiasthmatic; vasotropic.

XX Homo sapiens.

OS US2002110548-A1.

XX 15-AUG-2002.

XX 11-JUN-2001; 2001US-0878574.

XX 22-NOV-1996; 96US-0753233.

XX 03-DEC-1997; 97US-0984246.

XX 09-SEP-1998; 98US-0149674.

XX 14-JUN-1999; 99US-0333177.

XX (GEMY) GENETICS INST INC.

XX Sullivan F, Kriz R, Kumar R;

XX WPI; 2003-066673/06.

XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)

PT peptide, for manufacturing complex carbohydrates, or as targets for

PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant

PT rejection -

XX Disclosure; SEQ ID NO 13958; 6pp; English.

XX The invention relates to a composition comprising a human GDP-mannose

CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying

CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation

CC in a mammalian subject and for treating or ameliorating diseases affected

CC by the level of cellular fucosylation or diseases affected by the

CC fucosylation of glycoconjugates. These diseases include arthritis,

CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or

CC infection. The GM4,6D peptide or a polynucleotide encoding it is also

CC useful for manufacturing complex carbohydrates and as targets for

CC screening small molecule antagonists of the activity of the enzyme. The

CC polynucleotide is useful in developing an assay for defects in the

CC enzyme, as well as in gene replacement therapy. Sequences

CC ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding

CC human GM4,6D peptides of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format directly from USPTO

CC at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 256 BP; 61 A; 49 C; 65 G; 81 T; 0 other;

Query Match 13.6%; Score 158.2; DB 25; Length 256;

Best Local Similarity 76.9%; Pred. No. 9.5e-32;

Matches 193; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

515 TTCAATCAGGCAATGGCTGTGATCTCAGATGTTGAATGGCGTTAGAGATTGCAAT 574

6 TTCAATGAGGCTATGGCAAGTATCCGGAATAGTACTGGCACTCAAAATTGCACT 65

575 TGGGTCTTTGAGGGACTGGAAATCCATTGTGGATGTTGGTGGAACCTGGAATCACAGCA 634

66 TCAGTTTTTGGGGGCTAGATTCCATGCTGATGTTGGTGGAACCTGGAACCAACGCC 125

635 AAGATTATCTGTAGGCTTTTCCTAAGCTGAAATGCATGGTGTGGAACTGCCAAATGTT 694

126 AGAATTATCTGTAGGCTTTTCCTAAGTGAATGCTGTTGCTTGACCTTCCTCCCTGTT 185

695 GTGGAATTTGTCAGGAGCAACAAATTGACATTTGTTGGTGGGACATGTTTAAATGC 754

186 GTAGAACATTTGACAGGACCAATTAATTGAGTTTGTGGTGGTGCATGTTCAACTCT 245

755 ATCCCCAAGGC 765

Db 246 ATCCCTCAAGC 256

RESULT 10

ID ABX23518 standard; cDNA; 266 BP.

XX AC ABX23518;

XX 10-FEB-2003 (first entry)

XX Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #5575.

XX Human: GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;

XX cellular fucosylation; glycoconjugate fucosylation; transplant rejection;

XX arthritis; asthma; sepsis; reperfusion injury; stroke; infection;

XX complex carbohydrate; gene replacement therapy; immunosuppressive;

XX antiinflammatory; antiarthritic; antibacterial; cerebroprotective;

XX antiasthmatic; vasotropic.

XX Homo sapiens.

XX US2002110548-A1.

XX 15-AUG-2002.

XX 11-JUN-2001; 2001US-0878574.

XX 22-NOV-1996; 96US-0753233.

XX 03-DEC-1997; 97US-0984246.

XX 09-SEP-1998; 98US-0149674.

XX 14-JUN-1999; 99US-0333177.

XX (GEMY) GENETICS INST INC.

XX Sullivan F, Kriz R, Kumar R;

XX WPI; 2003-066673/06.

XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)

PT peptide, for manufacturing complex carbohydrates, or as targets for

PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant

PT rejection -

XX Disclosure; SEQ ID NO 5577; 6pp; English.

XX The invention relates to a composition comprising a human GDP-mannose

CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying

CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation

CC in a mammalian subject and for treating or ameliorating diseases affected

CC by the level of cellular fucosylation or diseases affected by the

CC fucosylation of glycoconjugates. These diseases include arthritis,

CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or

CC infection. The GM4,6D peptide or a polynucleotide encoding it is also

CC useful for manufacturing complex carbohydrates and as targets for

CC screening small molecule antagonists of the activity of the enzyme. The

CC polynucleotide is useful in developing an assay for defects in the

CC enzyme, as well as in gene replacement therapy. Sequences

CC ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding

CC human GM4,6D peptides of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format directly from USPTO

CC at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 266 BP; 91 A; 42 C; 60 G; 73 T; 0 other;

Query Match 12.3%; Score 142.8; DB 25; Length 266;

Best Local Similarity 72.1%; Pred. No. 1.1e-27;

Matches 186; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

701 AATTTCAGGACCAACAAATTTGACATTTGTTGGGGACATGTTTAAATCATCCCC 760

Db 2 AACTGACAGGACCAATAATTGAGTTTCTGTTGGTGACATGTTCAACTCTATCCCT 61
 Qy 761 AAGCTGATGAGTTCGCTTAATGTTTACATAATGGAAGCAACGATTGCGATG 820
 Db 62 CAAGCTGATGAGTTCGCTTAATGTTTACATAATGGAAGCAACGATTGCGATG 121
 Qy 821 AAGATATTAGAAAATTGTAAAGAGCTATTTCAGGTGAAAGCAACGAGAAAGTAGTT 880
 Db 122 AAGATCTGCAAAAGTGTAGAGATCTATTTCAGCAAGGCAACAGTGGAAAGTGATT 181
 Qy 891 GTCATAGATCTGTGATAAAGCAAAACAAAGATGAGCGCCCAAGTTACTGAACTAAAGCTC 940
 Db 182 ATCATAGATGCGTAATAAATGAGAAGCTAGATGACCGGATATGACACAAACAAAGCTT 241
 Qy 941 CTTATGGAATGACACATG 958
 Db 242 AGTTTGGACATTATTATG 259

RESULT 11

ABX19667
 ID ABX19667 standard; cDNA; 381 BP.
 XX AC
 XX ABX19667;
 DT 10-FEB-2003 (first entry)
 XX DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1724.
 XX KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
 KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
 KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
 KW complex carbohydrate; gene replacement therapy; immunosuppressive;
 KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
 KW antiasthmatic; vasotropic.
 XX OS Homo sapiens.
 XX PN US2002110548-A1.
 XX PD 15-AUG-2002.
 XX PF 11-JUN-2001; 2001US-0878574.
 XX PR 22-NOV-1996; 96US-0753233.
 XX PR 03-DEC-1997; 97US-0984246.
 XX PR 09-SEP-1998; 98US-0149674.
 XX PR 14-JUN-1999; 99US-0333177.
 XX PA (GBMY) GENETICS INST INC.
 XX PI Sullivan F, Kriz R, Kumar R;
 XX DR WPT; 2003-066673/06.
 XX PT New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
 XX PT peptide, for manufacturing complex carbohydrates, or as targets for
 XX PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant
 XX PT rejection
 XX FS Disclosure; SEQ ID NO 1726; 6pp; English.
 XX CC The invention relates to a composition comprising a human GDP-mannose
 CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
 CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
 CC in a mammalian subject and for treating or ameliorating diseases affected
 CC by the level of cellular fucosylation or diseases affected by the
 CC fucosylation of glycoconjugates. These diseases include arthritis,
 CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
 CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
 CC useful for manufacturing complex carbohydrates and as targets for
 CC screening small molecule antagonists of the activity of the enzyme. The
 CC polynucleotide is useful in developing an assay for defects in the

CC enzyme, as well as in gene replacement therapy. Sequences
 CC ABX17942-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding
 CC human GM4,6D peptides of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html.
 XX XX
 SQ Sequence 381 BP; 109 A; 88 C; 69 G; 115 T; 0 other;
 Query Match 12.3%; Score 142.2; DB 25; Length 381;
 Best Local Similarity 66.9%; Pred. No. 1.8e-27;
 Matches 236; Conservative 0; Mismatches 108; Indels 9; Gaps 2;
 Qy 21 CATTAAACAATGCCCTTAAGCAAGTGAAGTATTTTCAAGGTCAAGCTCTCTGTACAAAC 80
 Db 25 CTTCAATGAATAACCAAAAGAAATTGAGCTCTTTGAGGGCCAATCTCTCTGTACATGC 84
 Qy 81 ATTTGCTTGGCTTCATAGATTCTTAAGTGTCTAAATGGATGGTTTGAGCTTGACATACCCG 140
 Db 85 AGCTATATGGGACCTTAAGACCTATGTCTTAAAGTGGGCTGTCAACTAGGTATTCCAG 144
 Qy 141 ACATAATCCACAGCCATGACCATGGCCAAACCCCAATTTTTCAGAGTTGGTGTCAATTC 200
 Db 145 ACATAAT-----ACAGAACCATGCCAAACCCCAATTTCTCTTCTGACTTGGTCTTACTC 198
 Qy 201 TACAGTCCCACTAAACTTAACTCGTCAGTGCAGAGCCCTCATGCGTTATCTAGGCACACA 260
 Db 199 TTCAAATTCACCAGCTTAACGCTGCTTTGTGAGCGGTTTCATGCGCTTTTGGCACACA 258
 Qy 261 ATGGATTCTTTGAGATAGTAGTAAGTAATCCATGACAAACATAGA---AGCATATGCTCTCACTG 317
 Db 259 ATGGAATCTTTGAGATCCATGAGAGCCCAAGAGATCATGAACATAACATATGCTTAACCC 318
 Qy 318 CTGCTTCAGAGTTACTTTGTCAAAAGCAGTGAGCTTAGTTAGTCCAAATGGTT 370
 Db 319 CTGCATCAAAAGCTTCTTGTCAATAGTAGTATGATCATTTCTATCTCAATGGTT 371
 RESULT 12
 AAX25200
 ID AAX25200 standard; cDNA; 1412 BP.
 XX AC AAX25200;
 DT 19-JUL-1999 (first entry)
 XX DE Maize caffeic O-methyltransferase cDNA.
 XX KW Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant;
 XX KW ss.
 XX OS Zea mays.
 XX PH Key Location/Qualifiers
 XX CDS 139..1266
 XX FT /*tag= a
 XX FT /transl_except= (pos:817..819, aa:Ala)
 XX XX
 XX WO9910498-A2.
 XX PD 04-MAR-1999.
 XX PF 24-AUG-1998; 98WO-US17519.
 XX PR 12-MAY-1998; 98US-0076851.
 XX PR 27-AUG-1997; 97US-0057082.
 XX PA (PION-) PIONEER HI-BRED INT INC.
 XX PI Bowen BA, Helentjaris TG, Wang X;
 XX WPI; 1999-204667/17.
 XX DR P-PSDB; AAY05661.

XX Nucleic acids encoding plant lignin biosynthesis enzymes - used to
PT transform plants to modulate lignin biosynthesis
XX
PS Claim 2; Page 119-121; 166pp; English.
XX

CC This DNA sequence encodes a caffeic O-methyltransferase (see AAY05661)
CC of maize. A polynucleotide having this sequence can be amplified
CC from a cDNA library prepared from premeiotic to uninucleate tassel
CC from maize A632 using the primer pair given in AAX25225 and
CC AAX25226. The invention provides methods and compositions relating
CC to altering lignin biosynthesis and/or the lignin composition of
CC plants. Isolated nucleic acids (see AAX25196-216) that code for
CC proteins (see AAY05657-77) involved in lignin biosynthesis are
CC claimed. Also claimed are recombinant expression cassettes, host
CC cells (especially maize or sorghum), and transgenic plants and
CC seeds. The claimed nucleic acids can be used to transform a plant
CC to modulate lignin biosynthesis. A claimed method involves
CC transforming a plant cell with a recombinant expression cassette
CC comprising a lignin biosynthesis polynucleotide operably linked to
CC a promoter, growing the plant cell under plant growing conditions,
CC and inducing expression of the polynucleotide for a time sufficient
CC to modulate (preferably increase) lignin biosynthesis in the plant.
CC The plant lignins can be used as chemical feedstock. Plant
CC material of increased lignin content can be used as a fuel source,
CC and in the pulp and paper industry. Decreased lignin content
CC improves the digestibility of fodder crops.

XX SQ Sequence 1412 BP; 324 A; 400 C; 375 G; 313 T; 0 other;

Query Match 10.4%; Score 120.2; DB 20; Length 1412;
Best Local Similarity 54.0%; Pred. No. 1.8e-21;
Matches 292; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

QY 555 TGGCGTTTACAGATTGCAATTGGTCTTTCGAGGACTGGATCCATTGTGGATGGTGGTG 614
Db 734 TTGTCTGAGGGAGTGGCGGAGACGTTTCGTGGATCGACTCGTGGTGGAGCTCGGTG 793
QY 615 GTGGAACTGGAATCACAGCAAAAGATTATCTGTGAGGCTTTTCTTAAGCTGAAATGCATGG 674
Db 794 GTGGCATGTGGCGCGCGCCACCACATCGCCGCGCTTCCGCCACTCAAGTGGACGG 853
QY 675 TGTGGAACTCCAAATGTGTGGAAATTTGTGAGGAACAATTTGTCAGGAACAACAATTTGACATTTGGTTG 734
Db 854 TGCTTGACCTCCCGCACGTTGTGCGCGTGTCTCGTCTGATGGCAAGTTCGATCGTCG 913
QY 735 GTGGGACATGTTAATGATGATCCCAAGCTGATGAGTCTGCTTAAGTTGGTTTAC 794
Db 914 CAGGCAATATGTTGAGAGTATCCACTGCAACCGCTGTTTCTCAAGAAACTCTAC 973
QY 795 ATAATTGGAATGACACGATTGTCATGAAGATATTAGAAAATTGTAAGAAGCTATTTCAG 854
Db 974 ATGACTGGGTGACGATGAGTGTCTCAAGATATTGAAGATTGCAAGCAAGCCATATCTC 1033
QY 855 GTGAAGCAAAACAGGAAAGTAGTGTCTCATAGTACTGTGATGAACGAAACAAAGATG 914
Db 1034 CACGGGATGCGAGTGGGAAGTAAATAATCTTGGG---TGTGGTAGTGGATATAAAGT 1090
QY 915 AGCGCCAAAGTTACTGAAGTAAAGCTCTTATGGATGTACATGGCATGTATTATTAAATG 974
Db 1091 CAACATTAAGCATCAGAGACACAAGTATTGTTTATGTTTATGATGCGGGTTAAAG 1150
QY 975 GAAAGAGAGAGAGAGAGAGATTGGAGAAACTCTTCATGGAAGAGGGTTCCAAAGCT 1034
Db 1151 GAGTTGAGCGTGACGACAGAGATGGAGAGAGATCTTCACTGAAGCTGGATTCAAGACT 1210
QY 1035 ACAAAATATCTCCCTTACAGGATATTGTC---TCTTATGAGATCTATCTTGAATAC 1091
Db 1211 ACAAAATCTACCGCTCATTGGTATGATGATCGGTCATCATCGAGGTCTATCTCTGATGC 1270
QY 1092 T 1092
Db 1271 T 1271

RESULT 13
AAD19546
ID AAD19546 standard; cDNA; 1098 BP.
XX
AC AAD19546;
XX
DT 18-DEC-2001 (first entry)
XX
DE Medicago sativa caffeoyl CoA 3-O-methyltransferase (CCOMT) cDNA.
XX
KW Alfalfa; caffeoyl CoA 3-O-methyltransferase; CCOMT; lignin; woody plant;
XX forage legume; transgenic plant; paper industry; ss.
XX
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT CDS 1..1098
FT /tag= a
FT /product= "Alfalfa caffeoyl CoA 3-O-methyltransferase
FT (CCOMT) protein"
XX
PN WO200173090-A2.
XX
PD 04-OCT-2001.
XX
PF 23-MAR-2001; 2001WO-US09398.
XX
PR 24-MAR-2000; 2000US-192086P.
XX
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
XX
PI Dixon RA, Guo D;
XX
XX WPI; 2001-616527/71.
DR P-PSDB; AAEL2021.

XX Transforming forage legumes for modifying lignin composition and
PT increasing in vivo digestibility comprises transforming plants with
PT lignin biosynthetic enzyme genes under lignification-associated tissue
PT specific promoter -
XX
PS Example 1; Fig 6; 53pp; English.
XX
CC The invention relates to methods for producing forage legumes or woody
CC plants having altered lignin composition. Methods for transforming
CC forage legumes with a DNA construct comprises alfalfa caffeic acid 3-O-
CC methyltransferase (COMT), caffeoyl CoA 3-O-methyltransferase (CCOMT)
CC enzyme or its fragment under a lignification-associated tissue specific
CC promoter, resulting in the down regulation of the corresponding
CC homologous OMT genes either through antisense inhibition or sense
CC suppression. The methods are useful for down-regulation of the
CC corresponding homologous OMT genes, gene silencing, reduced OMT activity
CC levels, reduced lignin content, and modified lignin composition in
CC transgenic plants, and increased digestibility of transgenic plant
CC materials in ruminant animals. The expression of CCOMT transgene produces
CC an increased syringyl lignin to guaiacyl lignin ratio in the transformed
CC plant and greatly improved forage in vivo digestibility, and for making
CC lignins with altered dimer bonding patterns. Transforming forage legumes
CC with OMT enzymes is useful to produce plants having modified lignin
CC content and/or composition for direct comparison of the effects of lignin
CC content and/or composition for forage digestibility. The methods are also
CC useful for producing plants that are modified to alter lignins and
CC improve pulping characteristics for the paper industry. The present cDNA
CC sequence encodes alfalfa caffeoyl CoA 3-O-methyltransferase (CCOMT)
XX protein.

SQ Sequence 1098 BP; 324 A; 210 C; 240 G; 324 T; 0 other;

Query Match 10.2%; Score 118; DB 22; Length 1098;
Best Local Similarity 52.7%; Pred. No. 6.2e-21;
Matches 309; Conservative 0; Mismatches 265; Indels 12; Gaps 2;

AAC40707
ID AAC40707 standard; DNA; 1267 BP.
XX
AC AAC40707;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29270.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 08-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145513.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147835.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.

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PR 23-AUG-1999; 99US-0149902;
PR 23-AUG-1999; 99US-0149930;
PR 23-AUG-1999; 99US-0150566;
PR 26-AUG-1999; 99US-0150884;
PR 27-AUG-1999; 99US-0151065;
PR 27-AUG-1999; 99US-0151066;
PR 27-AUG-1999; 99US-0151080;
PR 30-AUG-1999; 99US-0151303;
PR 31-AUG-1999; 99US-0151438;
PR 01-SEP-1999; 99US-0151930;
PR 07-SEP-1999; 99US-0152363;
PR 10-SEP-1999; 99US-0153070;
PR 13-SEP-1999; 99US-0153758;
PR 15-SEP-1999; 99US-0154018;
PR 16-SEP-1999; 99US-0154039;
PR 20-SEP-1999; 99US-0154779;
PR 22-SEP-1999; 99US-0155139;
PR 23-SEP-1999; 99US-0155486;
PR 24-SEP-1999; 99US-0155659;
PR 28-SEP-1999; 99US-0156458;
PR 29-SEP-1999; 99US-0156596;
PR 04-OCT-1999; 99US-0157117;
PR 05-OCT-1999; 99US-0157753;
PR 06-OCT-1999; 99US-0157865;
PR 07-OCT-1999; 99US-0158029;
PR 08-OCT-1999; 99US-0158232;
PR 12-OCT-1999; 99US-0158369;
PR 13-OCT-1999; 99US-0159293;
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PR 13-OCT-1999; 99US-0159295;
PR 14-OCT-1999; 99US-0159329;
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PR 14-OCT-1999; 99US-0159331;
PR 14-OCT-1999; 99US-0159637;
PR 14-OCT-1999; 99US-0159638;
PR 18-OCT-1999; 99US-0159584;
PR 21-OCT-1999; 99US-0160741;
PR 21-OCT-1999; 99US-0160767;
PR 21-OCT-1999; 99US-0160768;
PR 21-OCT-1999; 99US-0160770;
PR 21-OCT-1999; 99US-0160814;
PR 21-OCT-1999; 99US-0160815;
PR 22-OCT-1999; 99US-0160980;
PR 22-OCT-1999; 99US-0160981;
PR 22-OCT-1999; 99US-0160989;
PR 25-OCT-1999; 99US-0161404;
PR 25-OCT-1999; 99US-0161405;
PR 25-OCT-1999; 99US-0161406;
PR 26-OCT-1999; 99US-0161359;
PR 26-OCT-1999; 99US-0161360;
PR 26-OCT-1999; 99US-0161361;
PR 28-OCT-1999; 99US-0161920;
PR 28-OCT-1999; 99US-0161922;
PR 28-OCT-1999; 99US-0161993;
PR 29-OCT-1999; 99US-0162142;
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Query Match          9.8%; Score 114; DB 21; Length 1267;
Best Local Similarity 54.9%; Pred. No. 7, 3e-20;
Matches 225; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

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Qy 554 TTGGCGTTTAGAGATTGCAATGGTCTTTTCAGGCACTGGAATCCATTCGATGTTGGT 613
Db 638 AAGAAGATCTTGAAGACCTATAAGGGTTTGAAGGATTCACCTCTTTGGTTGATGTTGGT 697

Qy 614 GGTGGAACCTGGAACACAGCAAGAAATATCTGTGAGGCTTTTCCTAAGCTGAAATGCATG 673
Db 698 GTTGGCATTGTGTCTACACTCAAAATGATTCCTCCAAAGTACCCCTAATCTTAAAGGCATC 757

Qy 674 GTGTGGAACGCTCCAAATGTTGTGAAAAATTTGTGAGGAAGCAACAATTTGACATTTGTT 733
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Search completed: November 9, 2003, 23:45:31
Job time : 432 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 23:36:54 ; Search time 102 Seconds
(without alignments)
5019.651 Million cell updates/sec

Title: US-09-868-547-3

Perfect score: 1160

Sequence: 1 gtttgctattaggcttctt.....ataaaagtattctgtgt 1160

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	109.8	9.5	1368	2	US-08-204-288-1
3	109.8	9.5	1503	2	US-08-715-325-1
4	109	9.4	1507	4	US-09-453-323-1
5	108	9.3	1244	2	US-08-204-288-3
6	107.8	9.3	1370	4	US-09-500-569-3
7	97	8.4	1430	2	US-08-204-288-4
8	95.4	8.2	1195	4	US-09-500-569-11
9	94.6	8.2	1380	3	US-08-991-677-5
10	92.6	8.0	1630	4	US-09-615-192A-107
11	89.6	7.7	381	4	US-09-615-192A-174
12	86.2	7.4	661	4	US-09-615-192A-127
13	86.2	7.4	744	2	US-08-975-316-51
14	86.2	7.4	744	4	US-09-615-192A-51
15	82.6	7.1	1471	2	US-08-204-288-6
16	81.6	7.0	1525	1	US-08-186-833-3
17	74.6	6.4	1308	4	US-09-500-569-13
18	70.2	6.1	1458	4	US-09-500-569-15
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20	61.8	5.3	1342	4	US-09-500-569-9
21	60.6	5.2	470	4	US-09-615-192A-189
22	59	5.1	438	4	US-09-615-192A-187
23	57.8	5.0	1036	4	US-09-615-192A-191
24	57.2	4.9	7218	1	US-08-332-463-14
25	54.2	4.7	682	4	US-09-615-192A-192
26	53.6	4.6	760	4	US-09-500-569-7
27	47.8	4.1	849	4	US-09-500-569-25

28	45.8	3.9	1314	4	US-09-500-569-5	Sequence 5, Appli
29	40.6	3.5	1956	4	US-08-559-896B-1	Sequence 1, Appli
30	40.6	3.5	12886	4	US-09-453-702B-14	Sequence 14, Appl
31	40.2	3.5	1664976	4	US-08-916-421B-1	Sequence 1, Appli
32	38.2	3.3	289	3	US-09-007-005-17	Sequence 17, Appl
33	38.2	3.3	289	3	US-09-244-796-17	Sequence 17, Appl
34	38	3.3	202001	4	US-09-734-674-3	Sequence 1, Appli
35	37.6	3.2	319608	4	US-09-539-333D-1	Sequence 1, Appli
36	37.6	3.2	319608	4	US-09-679-403-1	Sequence 1, Appli
37	37.2	3.2	549	4	US-09-107-532A-2800	Sequence 2800, Ap
38	36.8	3.2	4892	4	US-09-620-312D-1065	Sequence 1065, Ap
39	36.6	3.2	993	4	US-09-134-001C-974	Sequence 974, App
40	36.6	3.2	5361	3	US-08-973-462-2	Sequence 2, Appli
41	36.6	3.2	6152	3	US-08-973-462-1	Sequence 1, Appli
42	35.2	3.0	4529	2	US-08-449-645A-16	Sequence 16, Appl
43	35.2	3.0	4529	2	US-08-702-367A-16	Sequence 16, Appl
44	35.2	3.0	4529	5	PCT-US95-04681-16	Sequence 16, Appl
45	35	3.0	35100	1	US-08-306-691B-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-500-569-17
; Sequence 17, Application US/09500569
; Patent No. 6329204

GENERAL INFORMATION:

; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BBI327 US NA
; CURRENT APPLICATION NUMBER: US/09/500,569
; CURRENT FILING DATE: 2000-02-09
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (472)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1156)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1180)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1262)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1302)
US-09-500-569-17

Query Match 9.8%; Score 114; DB 4; Length 1314;

Best Local Similarity 54.5%; Pred. No. 89-22;

Matches 228; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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QY	508	CAAGTCATTCATGAGGCAATGCTTGTCATCTCAGATGTTGAACCTTGCCTTTAGAGA	567
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QY	568	TTGCAATTGGGCTTTTGAGGGAATGGAATCCATTTGGGATGTTGGTGGTGAATGGAAT	627

Db 650 GACCTACACAGGCTTTGAGGCACTTAATCCCTGTTGATGTTGGTGGAGAACTGGAGC 709
QY 628 CACAGCAAAAGATTAATCTGTGAGGCTTTCTTAAGCTGAATGCAATGCAATGTTGGAACTGCC 687
Db 710 TGTAGTCAACATGATGTTCTCAAGATATCCCACTATTAAAGGGCAATTAATTTGATTTGCC 769
QY 688 AATGTTGTGMAAATTTGTCAGGAACAAATTTGACATTTGTTGGTGGGACATGTT 747
Db 770 CCATGTCATTGAAGATGCCCATCTTATCCAGGAGTGGAAATGTTGGTGGAGATATGTT 829
QY 748 TAAATGATCCCAAGGCTGATGCTGCTTAAGTTGGTTTACATAATTTGGAATGA 807
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QY 808 CAACGATTCATGAAGATATTAGAAATTTGTAAGAGAGCTATTTCAGGTGAAAGCAAA 865
Db 890 TGAGCACTGCTTGAAGTTTTTGAAGAACTGCTATGAGGCACCTACCAGATAATGGAAA 947

RESULT 2

US-08-204-288-1
; Sequence 1, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
; APPLICANT: VAN DOORSSLAERE, Jan
; APPLICANT: PRITIG, Bernard J.M.
; APPLICANT: INZE, Dirk G.
; APPLICANT: JOUANIN, Lise
; APPLICANT: KNIGHT, Mary E.
; APPLICANT: VAN MONTAGU, Marc
; APPLICANT: LEGRAND, Michel
; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBAY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9119279.9
; FILING DATE: 10-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01450
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-204-288-1

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Best Local Similarity 49.6%; Pred. No. 1.1e-20;
Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps 1;

QY 448 ATTGAGGCTCTCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCTCATATAA 507
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QY 568 TTGCAATGGGCTTTTGAGGAGCTGAATCCATTGTGGATGTTGGTGGTGGAACTGGAAT 627
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QY 808 CAACGATTCATGAGATATTAGAAAATTTGTAAGAAGCTATTTCAGGTGAAAGCAAAAC 867
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QY 868 AGGAAAAGTAGTTGTCATGATACCTGTGATAACGAAAACAAAGATGAGCGCCAGTTAC 927
Db 927 GATACTTGTGTAGTGCATTTCTCCCGTGGCTCTGACACAAGCCTTGCACCAAGGG-- 983
QY 928 TGAACCTAAAGCTCTTATGATGCTACACATGGCATGATATTATTAATGGAAGAGAGAAA 987
Db 984 ---AGTCGTTCACTGATGTTATCATGCTGGCGCACACCCCGTGGGAAAGAGAGGAC 1040
QY 988 AGAAGAAGATTGGAAGAACTCTTCAATGGAAGCAGGGTTCCAAAGCTACAAAATATCTCC 1047
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QY 1048 CTTACAGGATATTCTCTCTTATTGAGATC 1078
Db 1101 CTGTGCAATTCAACACACATGTCATTTGAATC 1131

RESULT 3

US-08-715-325-1
; Sequence 1, Application US/08715325
; Patent No. 5886243
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Tsai, Chung-Jui
; APPLICANT: Podila, Gopi
; TITLE OF INVENTION: Genetic Engineering of Wood Color
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael, Best & Friedrich
; STREET: 100 E. Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: United States of America
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS 6.22
; SOFTWARE: WordPerfect for Windows 5.2

APPLICANT: VAN DOORSSELAERE, Jan
APPLICANT: PRITIG, Bernard J.M.
APPLICANT: INZE, Dirk G.
APPLICANT: JOUANIN, Lise
APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: CUSHMAN DARBAY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1244 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-204-288-3

Query Match 9.3%; Score 108; DB 2; Length 1244;
Best Local Similarity 52.6%; Pred. No. 3.5e-20;
Matches 259; Conservative 0; Mismatches 230; Indels 3; Gaps 1;
QY 404 TGNACCACTTTGAGAGGTGGTTCATGAGGAAGATCTCAGATATTGAGGTCTCCTTA 463
Db 268 TGTACCACTTAAAGATGACGATGAGTGGTGAATCCCATTCACAAAGCCCTATGGA 327
QY 464 GGAACACCTTTCTGGGACTTTATCAATAAGACCCCTGCATATACAAAGTCATCAATGAG 523
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QY 524 GCAATGCTTGTGATTTCTCAGATGTTGAACCTTGGCGTTTGTAGAGATTGCAATTTGGTCTTT 583
Db 385 GGAATGCTGATCACTCCCATGATGCAATGAAAAGATTCTTGAGGACTACAAGGATTT 444
QY 584 GAGGACTGGATCCATTTGGATGTTGGTGGTGGAACTGGAATCAAGCAAGATTAATC 643
Db 445 GAAGGCTTAATTCATTTGATGTTGGTGGTGGAACTGCGCTACTGTTAACATGATT 504
QY 644 TGTGAGGCTTTTCTTAAGCTGAATGATGTTGGTGGTGGAACTGCGCTACTGTTAACATGATT 703
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QY 704 TTGTCCAGGAAGCAACAATTTGACATTTGTTGGTGGGACATGTTAAATGCATCCCCAAG 763
Db 565 GTCCAGCTTACCTCGTGTGAGACAGCTTGTGGGACATGTTTCCAGTGTGCCAAAA 624
QY 764 GTGATGCAAGTTCTGCTTAAGTTGTTTACATAAATTGGAATCACAACGATTTCATGAAG 823
Db 625 GCAGATGCCATTTTCATGAGTGGATTGTCATGTTGGAGCGACGAGCATTTGCCAAAA 684
QY 824 ATATTAGAAAATTTGTAAGAGCTATTTCAGGTGAAGCAAAAACAGAAAAGTAGTTGTC 883
Db 685 TTCTTGAAGAAATTCCTATGAAGCACTACCTGCAATGGGAAGGTGATAATAGCGAGTGC 744
QY 884 ATAGATACTGTG 895
Db 745 ATACTCCAGAG 756
RESULT 6
US-09-500-569-3
; Sequence 3, Application US/09500569
; Patent No. 6329204
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BE1327 US NA
; CURRENT APPLICATION NUMBER: US/09/500,569
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,587
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1370
; TYPE: DNA
; ORGANISM: Glycine max
US-09-500-569-3

Query Match 9.3%; Score 107.8; DB 4; Length 1370;
Best Local Similarity 50.9%; Pred. No. 4.1e-20;
Matches 315; Conservative 0; Mismatches 292; Indels 12; Gaps 2;
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Db 523 GAAGAGGATTTCCATTTAACAGGCTTATGGAATGACAGCCTTTGAGTACCATGGAACA 582
QY 494 GACCTGCAATATAACAAGTCATTCAATGAGGCAATGGCTTGTGATTTCTCAGATGTTGAAC 553
Db 583 GATCCAAGGTTTAAACAAGGTTTTCACAAGGGAATGGCTGATCACTCTACCATCACAATG 642
QY 554 TTGGCGTTTAGAGATTGCAATGGGTCTTTGAGGAGTGGAAATCCATTTGGATGTTGGT 613
Db 643 AAGAAAATTTCTTGAGACCTACACAGGTTTGTAGAGTCTTAAATCTCTGGTGTGATGTTGT 702
QY 614 GGTGGAACCTGGAATCACAGCAAGATTTCTGTGAGGCTTTTCTTAAGCTGAAATGCAATG 673
Db 703 GGTGGAACCTGGAATCACAGCAAGATTTCTGTGAGGCTTTTCTTAAGCTGAAATGCAATG 762
QY 674 GTGTTGGAACCTGGAATTTGTTGGAATTTGTTCAGGAAGCAACAATTTGACATTTGTT 733
Db 763 AATTTTGAATTTGCTCATGTCATTTGAAGATGCCCATCTTATCTCGAGTGGAGCATGTA 822
QY 734 GGTGGGACATGTTTAAATGCATCCCAAGGCTGATGAGTCTGCTTAAGTGGTGTGTTA 793
Db 823 GGTGGAGATGTTTTCGAGTGTTCGAAAGCTGATGCTATTTTATGAGTGGATTTGC 882
QY 794 CATPATTGGAATCACAAACGATTGCAAGATATTAGAAAATTTGTAAAGAGCTATTTC 853
Db 883 CAGCATTTGAGTGTGAGCCTGCTTTGAAAGTTTGTGAAAGCTGCTACGAGGCACTACCA 942
QY 854 GGTGAAAGCAAAACAGGAAAAGTAGTTGTCAATGATGATGATAAAGCAAAACAAAGAT 913

Db 943 G-----ACAATGGGAAGGTGATTTGGGAGAAAGCAATCTTCCAGTGGCTCCAGAC 993
Qy 914 GAGGCCAAAGTTACTGAACCTAAAGCTCTCTATGATGTACACA--TGGCATGTATTATT 970
Db 994 TCTAGCTTGGCCACAAAAGTGTGGTTCACATCATGATGATCATGTGGCACAATATCCA 1053
Qy 971 AATGGAAAAGAGAGAAAAGAGAGATTGGAAGAAACTCTTTTATGGAAAGCAGGTTCCAA 1030
Db 1054 CGTGGGAAAGAGAGAACAGAGAAAGAGTTTGAGGCTCTGGCCAAAAGGCTCTGGATTCAA 1113
Qy 1031 AGCTACAAAATATCTCCCT 1049
Db 1114 GGTTCGAGTTGTTGCT 1132

RESULT 7
US-08-204-288-4
; Sequence 4, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
; APPLICANT: VAN DOORSSSELARE, Jan
; APPLICANT: FRITIG, Bernard J.M.
; APPLICANT: INZE, Dirk G.
; APPLICANT: JOURNIN, Lise
; APPLICANT: KNIGHT, Mary E.
; APPLICANT: VAN MONTAGU, Marc
; APPLICANT: LEGRAND, Michel
; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,288
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9119279.9
; FILING DATE: 10-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01460
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1430 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-204-288-4

Query Match 8.4%; Score 97; DB 2; Length 1430;
Best Local Similarity 52.9%; Pred. No. 3.8e-17;
Matches 231; Conservative 0; Mismatches 205; Indels 1; Gaps 1;

Qy 459 CCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCCTGCATATAACAAGTCATTCA 518
Db 528 CCTATGGAATGCAAGCATTTGAGTACCATGCCACAGATCCAAAGATTCAAACAAGTGTTC 587
Qy 519 ATGAGGCAATGGCTTGTGATTCACAGATGTGAACCTTGGCGTTTATGAGATTGCAATGGG 578
Db 588 ACCGTGGAATGTCTGATCACTCCCACTATGTCAATGAAGAAGATCTTTGAGGACTACAAAG 647
Qy 579 TCTTTGAGGACTGGATCCATTTGATGTTGGTGGTGAACCTGGAATCACAGCAAGA 638
Db 648 GATTTGAGGCCCTAAATTCCTATTTGATGTTGGTGGTGAACGGGTGCTACTCTTTAACA 707
Qy 639 TTATCTGTGAGGCTTTTCTTAAGCTGAAATGCAATGCTGTTTGGAACTCCCAATCTTGTGG 698
Db 708 TGATTTGCTCTAAATATCCCTCTATTAAAGGCATTAACTTTGATTTGCCACATGTAATTG 767
Qy 699 AAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAATGCAATCC 758
Db 768 GAGATGCTCCAACTTACCCCGGTGTCAGCACCTTGGTGGCGACATGTTTGTAGTGT-G 826
Qy 759 CCAAGGCTGATGAGTTCTCTTAAGTTGTTTACATATTTGAAATGCAACAGCATTTGCA 818
Db 827 CCAAGCAGATGCCATTTTCATGAATGGATTTTGTCAATTTGGAGCGATGAGCATTTGCC 886
Qy 819 TGAAGATATTAGAAAATTTGTAAGAAGCTATTTCAAGTGAAGCAACAAACAGGAAAAGTAG 878
Db 887 TAAATTTCTTGAAGAATTTGCTATGAAGCACTACTCTCAATGGGAAGTGTATTAATTGCAG 946
Qy 879 TTGTCTAGATACTGTG 895
Db 947 AGTGCATACTTCCAGAG 963

RESULT 8
US-09-500-569-11
; Sequence 11, Application US/09500569
; Patent No. 6329204
; GENERAL INFORMATION:
; APPLICANT: Caboon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
; FILE REFERENCE: BB1327 US NA
; CURRENT APPLICATION NUMBER: US/09/500,569
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: 60/119,587
; EARLIER FILING DATE: 1999-February-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Glycine max
US-09-500-569-11

Query Match 8.2%; Score 95.4; DB 4; Length 1195;
Best Local Similarity 52.4%; Pred. No. 9.7e-17;
Matches 210; Conservative 0; Mismatches 191; Indels 0; Gaps 0;
Qy 464 GGAACACCTTTCTGGGACTTTATCAATAAAGACCCCTGCATATAACAAGTCATTCAATGAG 523
Db 502 GGAATAACACGTTTGAATATCCGACATGAACCTCGAGCTTCAATCAGCTTTTCATGGCA 561
Qy 524 GCAATGGCTTGTGATTTCTAGATGTTGAACTTGGCGTTTAGAGATTTGCAATTTGGGCTTTT 583
Db 562 GCTATGACAAACCGTGCAACTTTTAATAATGAAGAAGATTTTGAATCCTCAAGGGGTTT 621
Qy 584 GAGGGACTGGAATCCCATTTGTTGGATGTTGGTGGGAACTGGAATCACAGCAAGATTATC 643
Db 622 GACACCTCMTAGCTGTTGGTGGACGTTGGAGTGGCGCTTGGTGTACACTTACATAGTC 681
Qy 644 TGTGAGGCTTTTCTTAAGCTGMAATGATGTTTGGAAAGCTCCCAATGTTGTGGAATAAT 703

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Db 682 ACTTCTAAATACCTTCACATTAAGGCTATCAATTTTGACTTGGCCACATGTCATAGAAT 741
Qy 704 TTGTCAGAGCAACAATTTGACATTTGTTGGTGGGACATGTTTAAATGATCCCAAG 763
Db 742 GCCTCTACTATCCCTGGTGTGAGCATGTGGAGGAGATATGTTTGAAGTGTGCCAA 801
Qy 764 GCTGATCAGTCTCTCTTAAAGTGTGTTTACATAATTCGAATGACAACGATGTCATGAAG 823
Db 802 GGAGATGCCATTTGATGATGTGTACTTCAATGATGAGATGATGATGATGATGATGATG 861
Qy 824 ATATTAGAAATTTGTAAGAAGCTATTTTCAAGTGAAGCAA 864
Db 862 GTATTAAAGATTTGTTATGCTTCTATTCCTAGTATGAAA 902

RESULT 9
US-08-991-677-5
; Sequence 5, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Carraway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syngyl Lignin in Gymnosperms
; FILE REFERENCE: 50617
; CURRENT APPLICATION NUMBER: US/08/991,677A
; CURRENT FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: US 60/033,381
; EARLIER FILING DATE: 1996-12-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1170)
US-08-991-677-5

Query Match 8.2%; Score 94.6; DB 3; Length 1380;
Best Local Similarity 50.1%; Pred. No. 1.7e-16;
Matches 325; Conservative 0; Mismatches 309; Indels 15; Gaps 3;

Qy 404 TGAACACAGTTTGAAGAGTGGTTCATGAGGAAGATCTCAGATATTTGAGTCTCCTTA 463
Db 490 TGGTACCACTTGACCGAGGCGAGTCTTGAAGTGAATTCATTAAACAGGCCCTATGGA 549
Qy 464 GGAACACCTTTCTGGGACTTTTATCAATAAAGACCTCGATATAACAACTCAATCAATGAG 523
Db 550 ATGACAGCATTTGAGTACCATGGC---ACCGATCCAGATTCACACAGATTTTCAACAT 606
Qy 524 GCAATGGCTTGTGATCTCAGATTTGNACTTGGGTTTGAAGATGCAATGGGTCTTT 583
Db 607 GGAATGTCATATTCACCATTCACCATGAAGAAATTCCTTGAGACTTACAAAGGGTTC 666
Qy 584 GAGGACTGGAATCCATTTGATGATGTTGGTGGTGAATCTGGAATCAGACCAAGATATC 643
Db 667 GAGGACTTGAATCTGCTGTTGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 726
Qy 644 TGTGAGGCTTTTCTAAGCTGAAATGATGTTGTTGGAACCTCCAAATGTTTGGAAAAAT 703
Db 727 ATCGCTAAATACCCCATGATCAAGGCAATTAACCTTGCATTTGCTCATGTTATTGAGAG 786
Qy 704 TTGTCAGGAACAACAATTTGACATTTTGGTGGGACATGTTTAAATGATCCCAAG 763
Db 787 GCTCCCTCCTATCTCGTGTGGAGCATGTTGGTGGGATATGTTTGTAGTGTCCAAA 846
Qy 764 GCTGATCAGTCTCTGCTTAACTTGGTGTGTTTACATAATTTGGAATGACAGTATGATGAAG 823
Db 847 GGAGATGCCATTTTCATGAAGTGAATGTCATGATTTGGGCGGATGAACACTGCTTGAAG 906
Qy 824 ATATTAGAAATTTGTAAGAAGCTATTTTCAAGTGAAGCAAAAACAGGAAAAAGTAGTTGTC 883
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Db 907 TTTTGAAGAAATTTTATGAAGCACTTCCA-----ACCAATGGGAAGGTGATCCTT 957
Qy 884 ATAGATACTGTGATTAACGAAACAAAGATGAGCGCAAGTTACTGAACTAAAGCTCCTT 943
Db 958 GCTGAATGCATCTCTCCCGTGGCCGAGACGCAAGCTCCCACTAAGGAGTGGTCAAT 1017
Qy 944 ATGATGTACACA---TGGCATGTATTTAATGAAAAAGAGAGAAAGAAAGATTTGG 1000
Db 1018 ATTGATGTCTATGTTGGTCTATAACCCAGTGGGAAAGAGAGAACTGAGAAGGATTT 1077
Qy 1001 AAGAACTCTTCATGGAAGCAGGTTCCAAAGCTTACAAATATCTCCT 1049
Db 1078 GAGGCTTGGCCAGGGGCTGGATTTGAAGGTTTCCGAGTAGTACCT 1126

RESULT 10
US-09-615-192A-107
; Sequence 107, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bliksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; MODIFICATION OF PLANT LIGNIN CONTENT
; FILE REFERENCE: 11000.1003C4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-107

Query Match 8.0%; Score 92.6; DB 4; Length 1630;
Best Local Similarity 50.8%; Pred. No. 6.3e-16;
Matches 280; Conservative 0; Mismatches 259; Indels 12; Gaps 2;

Qy 494 GACCTGCAATTAACAAGTCAATCAATGAGCAATGCTTGTGATCTCAGATGTTCAAC 553
Db 576 GACCGCGATTCAACAAGATCTTTAACCGGGGATGTCGATCACCCACCATTAATG 635
Qy 554 TTGGCTTTAGAGATTGCAATTTGGTCTTTGAGGACTGGAATCCATTTGGATGTTGGT 613
Db 636 AAGAAGATATCTGAAACATACAAGGGCTTCGAGGGCTCGAGACCGTGGTGGATGTCGA 695
Qy 614 GGTGGAACCTGGAATCAGCAAGATTTATCTGTGAGGCTTTTCTAAGCTGAATGATG 673
Db 696 GGGGCACTGGGCGCTGCTCAGCATGATGTTGCCAATACCCATCGATGAAGGGATC 755
Qy 674 GTGTTGGAACCTGCAATTTGTGGAATTTTGTGAGGAACCAATTTGACATTTGTT 733
Db 756 AACTTCGACCTGCTCAGGTGATTGAAGCGCTCCACCCCTTCTGTTGTCAGCAGCTC 815
Qy 734 GGTGGGACATGTTTAAATGCAATCCCAAGGCTGATGTCAGTTCCTGTTAAGTTGGTTTA 793
Db 816 GGAGGGACATGTTCTGTCAGCGTTCCAAAGGGAGATGCCATTTTCATGAAGTGAATGC 875
Qy 794 CATAAATTTGGAATGCAACGATTCATGCAATATTAGAAAATTTGAAAAGACTATTTC 853
Db 876 CATGATGAGTGAACCAATTTGCGGAAATTTCTCAAGAACTGCTACGATGCGCTTCC- 934
Qy 854 GGTGAAAGCAAAACAGAAAAGTAGTTGTGATAGATCTGTGATAAACGAAAAACAAGAT 913
Db 935 -----CAACATGGAAGGTGATCGTTGAGAGTGGTACTCCTCTGTGTACCCAGAC 986
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QY 914 GAGGCCAAGTTACTGAACAAAGCTCCTTATGGATGTACACA---TGGCATGTATTATT 970
Db 987 ACGAGCCTAGGACCAAGAATGTATCCATCGACTGCATCATGTGTGGCCACACACCA 1046
QY 971 AATGGAAAGAGAGAAAGAGAGATTGGAGAAACTCTTCATGGAAGAGAGGTTCCAA 1030
Db 1047 GCGGGAAGAGAGACACAGAGAGGTTGAGGCAATTGGCCAAAGGGGCGGATTTCCAG 1106
QY 1031 AGCTACAAAT 1041
Db 1107 GCTTCCAAAT 1117

RESULT 11
US-09-615-192A-174
; Sequence 174, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-174

Query Match 7.7%; Score 83.6; DB 4; Length 381;
Best Local Similarity 58.8%; Pred. No. 2.5e-15;
Matches 174; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 617 GGAACCTGAATCAGCAGCAAGATTTATCTGTGAGGCTTTTCTTAAGCTGAAATGCAATGGT 676
Db 10 GAAATGGAACACACGGCCACCAAGCCATCGCGAAACGCTTTCGCATATGGAATGCACTATA 69
QY 677 TTGAAACGTCCAAATGTGTGAAAAATTTGTCAGGAACCAACATTTGACATTTGTTGGT 736
Db 70 TTTGATCTTCGCGATGTGTGCGCCAAATTTAGAAAGTTAGCAAGCTGAGATGTGTTGCT 129
QY 737 GGGACATGTTTAAATGCATCCCAAGCTGATGAGTTCTGCTTAAGTTGTTTACAT 796
Db 130 GGGACATGTTTGAATGCTTACCCAGCAGATGCAATTAATTAAGTGGATCTCCAT 189
QY 797 AATTGGAATGCAACGATTCATGAAGATATTAGAAAAATTTAGAAAGCTAT---ITCA 853
Db 190 GATTGGAGCGATGAAGCGCTGGAAGATCTGAGCGATGCAAGAGGCTTTAGGCAAG 249
QY 854 GGTGAACCAACACGGAAGATGTTGTCATAGATCTGTGTAACAGAAACAA 909
Db 250 GCGAAGGCAAGAAACAGAGGTTAATTAATGATGATGTTGATGCAACACGAA 305

RESULT 12
US-09-615-192A-127
; Sequence 127, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
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; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615.192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 127
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-615-192A-127

Query Match 7.4%; Score 86.2; DB 4; Length 661;
Best Local Similarity 52.3%; Pred. No. 2.6e-14;
Matches 190; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 502 ATATACAAAGTCATTCATGAGCAATGGCTTGTGATCTTCAGATGTTGAACCTGGCGTT 561
Db 94 ATTCAACACAGATTTTCAACAGGGCTATGCTGAGAATTTCTACCATGTTGATGAACAAGAT 153
QY 562 TAGAGATTGCAATTTGGGCTCTTTGAGGCACTGGAAATCCATTTGCGATGTTGGTGGGAAC 621
Db 154 TTTGATACCTTACGAGGTTTAAAGAGGTTTCAAGGTTTGGTGGATGTTGGAGAGGTAT 213
QY 622 TGGAAATCAGACAAAGATTTATCTGTGAGGCTTTTCTTAAGCTGAAATGCAATGCTGTTGA 681
Db 214 TGGGTGACTCTCAATCTCATAGTGTCTAGTATCCCCACATTTTCAGSAATCAACTTCGA 273
QY 682 AGTCCAAATTTGTGAAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGA 741
Db 274 CTTGTCCCATGCTGCTGCCGATGCTCTCACTACCCAGCTGTGAAACATGTTGGGTGGAGA 333
QY 742 CATGTTTAAATGCATCCCCAAGGCTGATGAGTTCTGCTTAAGTTGTTTACATAATTG 801
Db 334 CAAGTTTATAGTGTACCAAGTGGCCAGCTATTTTATGAAGTGGATTTGCAATGATTG 393
QY 802 GAATGCAACAGATTCATGATGAAGATATTAGAAAAATTTAGAAAAAGCTATTTTCAGGTGAAAG 861
Db 394 GAGCGATGATCATTCGAGGAAGCTTTTGAAGAATTTGCAAGGCGTTGCCAGAGAGGG 453
QY 862 CAA 864
Db 454 GAA 456

RESULT 13
US-08-975-316-51
; Sequence 51, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N., HAVUKKALA, Ilkka
; APPLICANT: and GRIERSON, Alastair W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: November 10, 2003, 01:02:50 ; Search time 461 Seconds
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Title: US-09-868-547-3
Perfect score: 1160
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: .2141354 seqs, 1595478879 residues
Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA: *
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: *
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq: *
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq: *
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq: *
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq: *
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq: *
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158.2	13.6	256	10	US-09-878-574-13958
2	142.8	12.3	266	10	US-09-878-574-5577
3	142.2	12.3	381	10	US-09-878-574-1726
4	120.2	10.4	1412	12	US-10-361-460-23
5	111.8	9.6	377	10	US-09-878-574-3502
6	111.6	9.6	1315	12	US-10-361-460-24
7	109.8	9.5	1503	10	US-09-947-027-5
8	109.8	9.5	1503	13	US-10-091-009-5
9	109	9.4	279	10	US-09-878-574-10987
10	108	9.3	1460	12	US-09-129-298-3
11	107.6	9.3	272	10	US-09-878-574-13211
12	107.4	9.3	1418	12	US-09-129-298-4
13	106.8	9.2	1306	12	US-10-361-460-25
14	100.2	8.6	1149	10	US-09-938-842A-2582
15	94.6	8.2	1380	9	US-09-796-256A-5
16	92.6	8.0	1630	15	US-10-174-693-107

17	89.6	7.7	381	15	US-10-174-693-174	Sequence 174, App
18	86.2	7.4	561	15	US-10-174-693-127	Sequence 127, App
19	86.2	7.4	744	15	US-10-174-693-51	Sequence 51, Appl
20	84	7.2	221	10	US-09-878-574-7401	Sequence 7401, Ap
21	82.2	7.1	2096	14	US-10-137-036-60	Sequence 60, Appl
22	82.2	7.1	3070	14	US-10-137-036-113	Sequence 113, App
23	81.6	7.0	1494	14	US-10-253-971-5	Sequence 5, Appli
24	70.4	6.1	278	9	US-09-923-876-2383	Sequence 2383, Ap
25	63.8	5.5	279	10	US-09-878-574-9707	Sequence 9707, Ap
26	63.8	5.5	1440	12	US-10-289-757-43	Sequence 43, Appl
27	62.2	5.4	267	9	US-09-923-876-518	Sequence 518, App
28	61.6	5.3	398	10	US-09-878-574-48	Sequence 48, Appl
29	60.6	5.2	470	15	US-10-174-693-189	Sequence 189, App
30	59.2	5.1	687	14	US-10-213-473-25	Sequence 25, Appl
31	59	5.1	438	15	US-10-174-693-187	Sequence 187, App
32	57.8	5.0	1036	15	US-10-174-693-191	Sequence 191, App
33	57.6	5.0	736	14	US-10-213-473-27	Sequence 27, Appl
34	57	4.9	804	14	US-10-213-473-24	Sequence 24, Appl
35	56	4.8	1414	14	US-10-361-460-22	Sequence 22, Appl
36	54.6	4.7	1269	12	US-10-289-757-42	Sequence 42, Appl
37	54.4	4.7	1452	12	US-10-289-757-42	Sequence 42, Appl
38	54.2	4.7	682	15	US-10-174-693-192	Sequence 192, App
39	53.4	4.6	813	14	US-10-213-473-26	Sequence 26, Appl
40	52.6	4.5	254	9	US-09-923-876-1047	Sequence 1047, Ap
41	52.6	4.5	1455	12	US-10-289-757-150	Sequence 150, App
42	52.6	4.5	1457	12	US-10-289-757-41	Sequence 41, Appl
43	52	4.5	266	9	US-09-923-876-893	Sequence 893, App
44	51	4.4	1428	12	US-10-289-757-149	Sequence 149, App
45	51	4.4	1429	12	US-10-289-757-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-878-574-13958
; Sequence 13958, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401) B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 13958
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701068136H1
US-09-878-574-13958

Query Match	13.6%	Score 158.2	DB 10	Length 256
Best Local Similarity	76.9%	Pred. No. 9.2e+33		
Matches 193	Conservative	0	Mismatches 58	Indels 0
Gaps	0			
QY	515	TTCAATGAGCAATGCTTGTGATCTCAGAGTTGCACTTGGCGTTTACAGATTGCAAT	574	
Db	6	TTCAATGAGCAATGCTTGTGATCTCAGAGTTGCACTTGGCGTTTACAGATTGCAAT	65	
QY	575	TGGGCTTTTGGAGGCACTGGAATCCATTGTGGATTGTGGTGGCACTGGAATCAGCA	634	
Db	66	TCAGTTTTTGGGGGCTAGATTCCATGTGGATTGTGGTGGCACTGGAACACGGCC	125	
QY	635	AAGATTATCTGAGGCTTTTCTTAAGCTGAAATGATGGTGTGGAACGTCCTCAATGTT	694	
Db	126	AGAATTATCTGAGGCACTTCTTAAGTTGAAATGTTGTGCTTGACCTTCTCTCTGTT	185	

QY 675 TGTGGAACTGCCAAATGTTGTGGAAATTTGTGAGGAAGCAACAATTTGACATTTGTTG 734
Db 854 TGTGACCTCCCGCAGTTGTGCGCGTGTCTCGTGTGAGCAAGCTGCAGTTGCTG 913
QY 735 GTGGGACATGTTTAAATGATCCCCAAGGCTGATGAGCTTCTGCTTAAAGTTGGTTTAC 794
Db 914 CAGCAATATGTTTGAGAGTATCCACCTGCAACCGCTGTTTCTCAAGAAACTCTAC 973
QY 795 ATAATTCGAATGACAAGATGCTGATGAGATATTTAGAAATTTGTAAGAGAGCTATTTCAG 854
Db 974 ATGCTGGGTGACATGAGTGTCTCAAGATATTTGAAGATTTGCAAGCAAGCCATATCTC 1033
QY 855 GTGAAACAAACAGGAAAGTAGTGTCTCATAGTACTGTGATAAAGCAAAACAAAGATG 914
Db 1034 CACGGATGACGGTGGGAAGTAATAATCTTGA--TGTTGAGTTGGATATAAACAGT 1090
QY 915 AGCGCAAGTACTGAACCTAAAGCTCTTATGATGTACACATGCGCATGTATTATTAATG 974
Db 1091 CAACATPAAGCATCAAGAGACACAAGTTATGTTTGTATATGATGCGGTTAAAG 1150
QY 975 GAAAGAGAGAAAGAAAGATTTGGAAGAACTCTTCATGGAAGCAGGTTCCAAAGCT 1034
Db 1151 GAGTTGAGCTGACGACAGAGTGGAGAGATCTTCACTGAAGCTGGATTCAAAGACT 1210
QY 1035 ACAAATATCTCCCTTCCAGGATATTGTC---TCTTATTGAGATCTATCCTTGAATAC 1091
Db 1211 ACAAATTCACCGCTATTGGTGATGTATCGGTCATCATCGAGTCTATCTTGAATG 1270
QY 1092 T 1092
Db 1271 T 1271

RESULT 5

US-09-878-574-3502
; Sequence 3502, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3502
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-009-Q1-B1-H12
US-09-878-574-3502

Query Match 9.6%; Score 111.8; DB 10; Length 377;
Best Local Similarity 55.3%; Pred. No. 4.9e-20;
Matches 209; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
QY 494 GACCTGCATATAACAAGTCAATGAGGCAATGCGCTTGTGATCTCAGATGTTGAAC 553
Db 7 GATCCAGGTTTAAAGGTTTCAACAGGGGATGCTGATCACTCTACCAATTACAATG 66
QY 554 TTGCGCTTTAGAGATTCGAATGGTCTTTGAGGACTGGAATCCATTGTGGATTTGGT 613
Db 67 AAGAAATCTTGAGACCTACACAGGCTTTGAGGACTTAAATCCCTGGTTGATTTGGT 126
QY 614 GTGGAACTGGAATCACAGCAAGATTTATCTGTGAGGCTTTTCTTAAGCTGAATGCAATG 673
Db 127 GGAGAACTGGAGCTGTAGTCAACATGATTGTCTCAAAGTATCCCCACTATTAAAGGCATT 186

QY 674 GTGTTGAAAGCTCCAAATGTTGTGGAAATTTGTGAGGAAGCAACAATTTGACATTTGTT 733
Db 187 AATTTTGAATTTGCCCATGTTCATTGAAGATGCCCATCTTATCCAGGAGTGGACATGTT 246
QY 734 GTGGGGAATGTTTAAATGCAATCCCAAGGCTGATGCAAGTCTCTGTTAAAGTTGGTTTAA 793
Db 247 GTGGGAGATATGTTTGTCAAGTGTTCAAAAGCTGATGCTATTTTATGAAGTGGATTTC 306
QY 794 CATAAATGGAATGACAACGATTCATGAAGATATTAGAAATTTGTAAGAGACTATTTC 853
Db 307 CAGATTTGAGTGTATGAGCATGCTTGAAGTTTGAAGAACTGCTATGAGGCACTACCA 366
QY 854 GGTGAAAGCAA 864
Db 367 GATAATGGGAA 377

RESULT 6

US-10-361-460-24
; Sequence 24, Application US/10361460
; Publication No. US2003Q163839A1
; GENERAL INFORMATION:
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
; FILE REFERENCE: 0709
; CURRENT APPLICATION NUMBER: US/10/361,460
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/057,082
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)...(1160)
US-10-361-460-24

Query Match 9.6%; Score 111.6; DB 12; Length 1315;
Best Local Similarity 52.7%; Pred. No. 1.1e-19;
Matches 290; Conservative 0; Mismatches 254; Indels 6; Gaps 2;
QY 546 TGTGAACTTGGCGTTTAGAGATTGCAATTTGGGTCTTTGAGGAGCTGGAATCCATTTGTG 605
Db 622 TGATGCCAATTGTCTCAGGAGTGGCGGAGATGTTCTGTGGATCAACTCATTTGGTTG 681
QY 606 ATGTTGGTGGTGAACCTGGAATCACAGCAAGATTTATCTGTGAGGCTTTTCTTAAGCTGA 665
Db 682 ACGTGGCGGTGGGCATGTGTGCGCGCCGCCCATCGCGCTTCCCGCACGTCA 741
QY 666 AATGCAATGTTTGGAAACCTCCAAATGTTGTGAAAAATTTGTGAGGAAGCAACAATTTGA 725
Db 742 AGTGACAGCTGTGTGACCTCCGCGAGTTGTGCGCGTGTCTCATCTGATGGCAACGTGC 801
QY 726 CATTTGTTGGTGGGACATGTTTAAATGCAATCCCAAGGCTGATGAGTCTGCTTAAAGT 785
Db 802 AGTTCGTCAGGAAATATGTTTGAGAGTATTTCCACCTGCAACCGCTGTTTCTCTCAAGA 861
QY 786 TGGTTTTACATAATTGGAATGACACGATTCGATGAAGATATTAGAAATTTGTAAGAAAG 845
Db 862 AAACCTACATGACTGGGTGACGATGAGTGTGTCAAGATATTGAAGAAATTCGAAGCAAG 921
QY 846 CTATTTGAGGTGAAAGCAAAACAGGAAAGTAGTGTGTCTATAGATATCTGTGATAAAGAA 905
Db 922 CCATACCTCCAGGATGAGGTGGAAGTAAATCTTTGGA---CGTGGTAGTTGGAT 978
QY 906 ACAAGATGAGCGCCCAAGTTACTGAACCTCCTTATGATGTACACATGGCATGTA 965

Db 979 ATAAACAGCTCAAAATAAAGCATCAAGACACAAAGTTATGTTCCGATTTGATATGATGG 1038
QY 966 TTATTTAATGGAAGAGAGAGAAAGAGAGATTGGAAGAACTCTTCATGGAAGCAGGGT 1025
Db 1039 CCGTTAACGGAGTTGAGCGTGACGAGCAAGAGTGGAAGAAATCTTCGCCGAAGCCGGAT 1098
QY 1026 TCCAAAGCTACAAAATATCTCCCTTCACAGGATATTTGTCTC---TTATTGAGATCTATC 1082
Db 1099 TCAAAGACTACAAAATCTACCCGTCATTTGGTGACGTGTGGTCAATCGAGGTCTATC 1158
QY 1083 CTTGAATACT 1092
Db 1159 CTTGAATGCT 1168

RESULT 7
US-09-947-027-5
; Sequence 5, Application US/09947027
; Patent No. US20020124281A1
; GENERAL INFORMATION:
; APPLICANT: Li, Laigeng
; APPLICANT: Chiang, Vincent Lee C.
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: AldomT; GenBank accession number: X62096
US-09-947-027-5

Query Match 9.5%; Score 109.8; DB 10; Length 1503;
Best Local Similarity 49.6%; Pred. No. 3.8e-19;
Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps 1;

QY 448 ATTTGAGGTCCTCTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCCTGCATATAA 507
Db 523 ATTTAACHAGGCCCTATGGATGACTGCATTTGAATATCATGCGCAGGATCCAAGATTCAA 582
QY 508 CAAGTCATTCAATGAGGCAATGGCTTTGATCTCAGATGTTGAACCTTGGCGTTTAGAGA 567
Db 583 CAAGGTCCTTCAACAAGGGAATGTCTGACCACTTACCATTACCATTGAAGAAGATTCTTGA 642
QY 568 TTGCAATTGGGCTTTTGGAGGACTGGAATCCATTGTGATCTCAGATGTTGAACCTTGGCGTTTAGAGA 627
Db 643 GACCTACAAAGGCTTTGAGSCCTCAGTCTCTTGGTGATGTTGGTGGGACTGGAGC 702
QY 628 CACAGCAAAAGATTATCTGTAGGCTTTTCTTAAGCTGAAATGCAATGCTGTTTGGAACTGTC 687
Db 703 CGTCGTTAACCACTCGTCTCTAAATACCTTCAATCAAGGCAATTAATCTGATCTGCC 762
QY 688 AAATGTTGTGAAAATTTGTGAGGAAGCAACAATTTGATGTTTGTGGTGGGACATGTT 747
Db 763 CCAGCTCAATTGAGGATGCCCATCTTATCCCGGAGTGGAGCATGTTGGTGGCAGATGTT 822
QY 748 TAAATGCATCCCAAGGCTGATGAGTTCTGTTAAAGTTGTTTACATAATTCGAATGA 807
Db 823 TGTAGTGTGCCCAAGCAGATGCCGTTTTCATGAAGTGGATATGCCATGATTGGAGCGA 882
QY 808 CAACGATTGATGAAGATATTAGAAAATTTGAAAGAACTATTTTCAGGTGAAAGCAAAAC 867
Db 883 CGCCCACTGCTTAAATTTCTTGAGCAATTTGCTATGACGCGTTGCGGAAACGCGAAGGT 942
QY 868 AGGAAAAGTAGTTGTCATAGATCTGTGATTAACGAAACAAAGATGAGCGCCCAAGTTAC 927

Db 943 GATFACCTTTGAGTGCAATCTTCCGTTGGCTCTCTGACACAAAGCCTTGCACCAAGGG--- 999
QY 928 TGAACATAAGCTCTTATGATGTACATGCGCATGTATTATTAAATGAAAAGAGAGAAA 987
Db 1000 ---AGTCGTGCACGCTTGATGTATCATGCTGGCGCACACCCCGTGGGAAAGAGAGAC 1056
QY 988 AGAAGAGATTTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATATCTCC 1047
Db 1057 CGAAGAGGAATTTGAGGGCTTAGCTAAGGGAGCTGGCTTCCAGGTTTTTGAAGTAATGTG 1116
QY 1048 CTTTCACAGGATATTGTCTCTTATTGAGATC 1078
Db 1117 CTGTGCAATCAACACACATGTCAITGAATTC 1147

RESULT 8
US-10-091-009-5
; Sequence 5, Application US/10091009
; Publication No. US20020138870A1
; GENERAL INFORMATION:
; APPLICANT: Li, Laigeng
; APPLICANT: Chiang, Vincent Lee C.
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND
; TITLE OF INVENTION: COMPOSITION, AND
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/10/091,009
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 05/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: AldomT; GenBank accession number: X62096
US-10-091-009-5

Query Match 9.5%; Score 109.8; DB 13; Length 1503;
Best Local Similarity 49.6%; Pred. No. 3.8e-19;
Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps 1;

QY 448 ATTTGAGGTCCTCTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCCTGCATATAA 507
Db 523 ATTTAACHAGGCCCTATGGGATGACTGCATTTGAATATCATGCGCAGGATCCAAGATTCAA 582
QY 508 CAAGTCATTCAATGAGGCAATGGCTTTGATCTCAGATGTTGAACCTTGGCGTTTAGAGA 567
Db 583 CAAGGTCCTTCAACAAGGGAATGTCTGACCACTTACCATTACCATTGAAGAAGATTCTTGA 642
QY 568 TTGCAATTGGGCTTTTGGAGGACTGGAATCCATTGTGATGTTGGTGGGACTGGAAAT 627
Db 643 GACCTACAAAGGCTTTGAGGCGCTCAGTCTCTTGGTGATGTTGGTGGGACTGGAGC 702
QY 628 CACAGCAAAAGATTATCTGTAGGCTTTTCTTAAGCTGAAATGCAATGCTGTTTGGAACTGTC 687
Db 703 CGTCGTTAACCACTCGTCTCTAAATACCTTCAATCAAGGCAATTAATCTGATCTGCC 762
QY 688 AAATGTTGTGAAAATTTGTGAGGAAGCAACAATTTGATGTTTGTGGTGGGACATGTT 747
Db 763 CCAGCTCAATTGAGGATGCCCATCTTATCCCGGAGTGGAGCATGTTGGTGGCAGATGTT 822
QY 748 TAAATGCATCCCAAGGCTGATGAGTTCTGTTAAAGTTGTTTACATAATTCGAATGA 807
Db 823 TGTAGTGTGCCCAAGCAGATGCCGTTTTCATGAAGTGGATATGCCATGATTGGAGCGA 882
QY 808 CAACGATTGATGAAGATATTAGAAAATTTGAAAGAACTATTTTCAGGTGAAAGCAAAAC 867

Db 883 CGCCCACTGTTAAATCTTTGAAGATTCGTATGACGCTTGCCGGAACGCAAGT 942
QY 868 AGGAAAGTAGTTGTCTATAGATCTGTGATAACGAAACAAAGATGAGCGCCAGTTAC 927
Db 943 GATACCTTTGAGTGCAATCTCCCGTGGCTCTGACACAGCTTGCCACCAAGGG--- 999
QY 928 TGAACCTAAAGCTCTTATGATGTACATGCGATGTATTATTAATGGAAGAGAGAAA 987
Db 1000 ---AGTCGTGCACGTTGATGTATCATGTCTGGCGCACACACCCCGTGGGAAGAGAGAC 1056
QY 988 AGAAGAGATGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTTACAAATATCTCC 1047
Db 1057 CGAAGAGGAATTTGAGGGCTTAGCTAAGGAGCTGGCTTCCAAAGTTTGAAGTAATGTG 1116
QY 1048 CTTACAGAGGATTTTGCTCTTATTGAGATC 1078
Db 1117 CTGTGATTCACACACATGTCATTGAATTC 1147

RESULT 9

US-09-878-574-10987
; Sequence 10987, Application US/09878574
; Patent No. US200201105481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(13401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 10987
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701063901H1
US-09-878-574-10987

Query Match 9.4%; Score 109; DB 10; Length 279;
Best Local Similarity 64.6%; Pred. No. 2.4e-19;
Matches 179; Conservative 0; Mismatches 95; Indels 3; Gaps 1;
QY 158 AGCCATGGCCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCACAGTCCCACT 217
Db 2 AACCATGCCAAACCCATTCTCTTCTGACTTGGTCTCTACTCTTCAAAATCCACCAGCT 61
QY 218 AAAACTCGTCAGGTGCAGAGCCCTCATGCGTTTCTAGCACACAATGATTCCTTTGAGATA 277
Db 62 AAGCTTGCCTTTGTGAGCGGTTTCATGCGCTTCTTGGCACACAATGGAATCTTTGAGATC 121
QY 278 GTAAGAATCCATGACAACTAGTA---AGCATATGCTCTCTACTGCTTCCAGAGTTACTT 334
Db 122 CATGAGCGCCAAAGAGATCATGAACATATGCTCTCAACCCCTGATCAAGTTCTT 181
QY 335 GTCAAAGAGCTGAGCTTAGTTAGTCCAAATGCTGAGTATTTCTTGAACCAAAATGT 394
Db 182 GTCAATAGTAGTACTCATTTCTATCTTCCAAATGGTTCTAGCGTTTACCGATCCACTCGG 241
QY 395 CAAGGTGCATGGGAACAGTTGAAGAGGTGGTTTCATG 431
Db 242 AAGTTAATACCATCACITGGGGGAGTGGCTTCGTG 278

RESULT 10

US-09-129-298-3
; Sequence 3, Application US/09129298
; Publication No. US20030196218A1
; GENERAL INFORMATION:

; APPLICANT: Arntzen, Charles
; APPLICANT: Kipp, Peter B.
; APPLICANT: Kumar, Ramesh
; APPLICANT: May, Gregory D.
; TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
; TITLE OF INVENTION: to Effect Localized Genetic Changes in Plants
; FILE REFERENCE: 7991-023-999
; CURRENT APPLICATION NUMBER: US/09/129,298
; CURRENT FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/054,386
; EARLIER FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84)...(1178)
US-09-129-298-3

Query Match 9.3%; Score 108; DB 12; Length 1460;
Best Local Similarity 52.6%; Pred. No. 1.1e-18;
Matches 259; Conservative 0; Mismatches 230; Indels 3; Gaps 1;
QY 404 TGAACCCAGTTGAAGAGGTGGTTCATGAGGAAGATCTCACAGTATTGAGGGTCTCCTTA 463
Db 501 TGTACCCTTAAAGATGCAGTACTAGATGTGGTAATCCCATTCACCAAGGCTATGGA 560
QY 464 GGAACACCTTCTGGGACCTTTATCAATAAAGACCCCTGCATATAACAAAGTCATTCAATGAG 523
Db 561 ATGACAGACATTTGAGTACCATGGC---ACAGATCCAAAGATTCACAAAGTTTTCACCGT 617
QY 524 GCAATGGCTGTGATCTCTCAGATGTTGAACCTTGGCGCTTTAGAGATTGCAATGGGTCTTT 583
Db 618 GGAATGTCTGATCACTCCACTATGTCAATGAAAAAGATTTCTTGAGGACTACAAAGGATTT 677
QY 584 GAGGACTGGAATCCATTCGTGATGTTGGTGGGAACCTGGAATCACACAAGATTATC 643
Db 678 GAAGCCTAAATTCATTTGATGTTGGTGGGAACCTGGCGCTACTGTTAACATGATT 737
QY 644 TGTAGGCTTTTCTTAAGCTGAAATGCATGTTTGGAAACGTCCTCAAAATGTTGGGAAAT 703
Db 738 GTCTCCAAACATCCCTCTATTAAAGGATTAATCTTGATTTACCATGATGTTGAGAT 797
QY 704 TTGTGAGGAAGCAACAATTTGACATTTGTTGGTGGGACATGTTTAAATGCAATCCCAAG 763
Db 798 GCTCCAGCTTACCCCTGGTGTGAGCAGCAGTTGGTGGCGACATGTTGCCAGTGTGCCAAA 857
QY 764 GCTGATGCAAGTCTGCTTAAGTTGTTTACATAATTGGAATGGAAGCAACAGATAAGTAGTTGC 823
Db 858 GGAGATGCCATTTTCAAGAATGGAATTTGATGATTGGAGCGCAGGATTCCTCTAA 917
QY 824 ATATTAGAAAATTTGTAAGAAGCTATTTTCAGGTGAAAGCAAAACAGAAAAAGTAGTTGTC 883
Db 918 TTCTTGAAGAAATTTGTAAGAAGCTACTCTGCAATTTGGAAGGTGATAATAGCGAGTGC 977
QY 884 ATAGATCTGTG 895
Db 978 ATACTTCCAGAG 989

RESULT 11

US-09-878-574-13211
; Sequence 13211, Application US/09878574
; Patent No. US200201105481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 13211
LENGTH: 272
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701066773H1
US-09-878-574-13211

Query Match 9.3%; Score 107.6; DB 10; Length 272;
Best Local Similarity 66.8%; Pred. No. 5.6e-19;
Matches 171; Conservative 0; Mismatches 79; Indels 6; Gaps 1;

Qy 21 CATTAAACAATGGCGTAAACCAAGTGAAGATTTTCAAGTCAAGCTCTCTGTACAAAC 80
Db 11 CTTCAATGAATAACCAAAAGAAATTTGAGCTCTTTGAGGGCCAATCTCTCTGTACATGC 70
Qy 81 ATTTGCTTGGCTTCATAGTCTTAAGTCTTAAATGATGATGAGCTTGAAGTTCGACATACCG 140
Db 71 AGCTATATGGCACCTAAGACCTATGTCTTAAAGTGGGCTGTTCAACTAGGTATTCAG 130
Qy 141 ACATAATCCACAGCCATAGCCATGCCCAACCCATTACTTTTTCAGAGTTGGTGTCAATTC 200
Db 131 ACATPAT-----ACAGNCCCATGCCAAACCCATTCTCTTCTGACTTGTCTCTACTC 184
Qy 201 TACAAGTCCCACTAACTCGTCAGGTGCGAGCGCTCATCGCTTATCTAGCACACA 260
Db 185 TTCAATTCACCAGCTAAACGCTTGTGCGAGCGCTTTCATGGCTTCTTGGCACACA 244
Qy 261 ATGCAATCTTTGAGAT 276
Db 245 ATGCAATCTTTGAGAT 260

RESULT 12

US-09-129-298-4
Sequence 4, Application US/09129298
Publication No. US20030196218A1
GENERAL INFORMATION:
APPLICANT: Arntzen, Charles
APPLICANT: Kipp, Peter B.
APPLICANT: Kumar, Ramesh
APPLICANT: May, Gregory D.
TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
FILE REFERENCE: 7991-023-999
CURRENT APPLICATION NUMBER: US/09/129,298
PRIOR FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,386
PRIOR FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1418
TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: CDS
LOCATION: (59)...(1153)
US-09-129-298-4

Query Match 9.3%; Score 107.4; DB 12; Length 1418;
Best Local Similarity 52.9%; Pred. No. 1.6e-18;
Matches 231; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

Qy 459 CCTTAGGAACACCTTCTGGACCTTATCATTAAGACCTCGCATATAACAAAGTCATCA 518
Db 528 CCTATGGAATGACAGCATTTGATGACCATGCGACAGATCCAAAGATTCAACAAAGTGTCA 587

Qy 519 ATGAGCAATGGCTTGTGATTTCTCAGATGTTGAACCTTGGCGTTAGAGATTCGAATGGG 578
Db 588 ACCGTGAATGTTCTGATCACTCCACTATGTCATGAAGAAGATTTCTTGAGGACTACAAAG 647
Qy 579 TCTTTGAGGACTGGAATCCATTGATGTTGGTGTGGAACCTGGAATCACAGCAAGA 638
Db 648 GATTGAAGSCCTAAATTCATTGTTGATGTTGGTGTGGAACGGGTGCTACTGTTAACA 707
Qy 639 TTATCTGTGAGGCTTTTCTTAAGCTGAAATGCAATGCTGTTGGAACGTTCCAAATGTTTGG 698
Db 708 TGATTGCTCTAAATATATCCCTCTATTAAAGGCATTAACTTTGATTTGCCACATGTAATTG 767
Qy 699 AAAATTTGTCAGGAACCAAAATTTGACATTTGTTGTTGGTGGGACATGTTTAAATGCAATCC 758
Db 768 GAGATGCTCAACTTACCCCGGTGTCAGCACGTTGTTGTCGACATGTTTGTAGTGTGC 827
Qy 759 CCAAGGCTGATGAGTCTCTCTTAAGTTGTTTACATAATTGGAATGCAACCAATGCA 818
Db 828 CAAAGCAGATGCCATTTTCATGAGTGGATTTGTCTATGTTGAGCGATGAGCATTTGCC 887
Qy 819 TGAAGATTTAGAAAATTTGAAAGAGCTATTTCAAGTGAAGCAAAACAGGAAAAGTAG 878
Db 888 TAAATTTCTTGAAGAATTTGCTATGAAGCACTACCTGCAATGGGAAGGTGATAATTGCG 947
Qy 879 TTGTCATAGATACCTGTG 895
Db 948 AGTGCATCTTCCAGAG 964

RESULT 13

US-10-361-460-25
Sequence 25, Application US/10361460
Publication No. US20030163839A1
GENERAL INFORMATION:
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Wang, Xun
TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
FILE OF INVENTION: Biosynthesis and Uses Thereof
FILE REFERENCE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/057,082
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 1306
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (57)...(1154)
US-10-361-460-25

Query Match 9.2%; Score 106.8; DB 12; Length 1306;
Best Local Similarity 51.3%; Pred. No. 2.3e-18;
Matches 273; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

Qy 577 GGTCTTTGAGGAGTGGAAATCCATTGTTGGATGTTGGTGGAACTGGAATCACAGCAA 636
Db 650 GGTGTTCCGTGGGATCGACTCGTTGTCGACGTCGCGGTGGGCGCGTGGCGCCCGCG 709
Qy 637 GATTATCTGTGAGGCTTTTCCTTAAGCTGAAATGATGTTGGTGGAACTGTTGAAATGTTGT 696
Db 710 CACCATCGCGCGCATTCGCGCACGCTCAAGTCGACGCTGTTGACCTCCGCACTGTT 769
Qy 697 GGAATTTGTCAGGAAGCAAAATTTGACATTTGTTGTTGGTGGGACATGTTTAAATGCA 756
Db 770 CGCCGGTGTCTCCATCCGATGCTGCTGCGTGTGTTGCGGGCAATATGTTCCACAGAT 829
Qy 757 CCCCAAGGTGATGACAGTTCTGCTTAAGTTGTTTACATAATTGGAATGACAAACGATTG 816

Db 830 TCCACCTGCAACCCCGTTCCTTCAAGACAACCTCTATGTGACTGGGGTGACGACGAGTG 889
QY 817 CATGAAGATATTAGAAAATTGAAAGAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGT 876
Db 890 CATCAAGATATTGAAGATTGCAAGCAGCCATATCTCCACGGATGAGGGTGGGAAGGT 949
QY 877 AGTTGTCATGATACTGTGATAAAGCAAAACAAAGATGAGCGCCAAAGTTACTGAACTAAA 936
Db 950 GATAAATCATGACGCTGTGTAGTCGGGTATGGCGATGCAAAATGAAGCGCTTAGAGACACA 1009
QY 937 GCTCCTTATCGATGTACATGCGCATGTATTATTAATGGAAGAGAGAGAAAGAGAGA 996
Db 1010 AGTTATGTTGATTTGTTTANGATGGCGG---TCAATGGATGTCAGCGCGCAGCAGCAAGA 1066
QY 997 TTGGAAGAAACTCTTCATGGAAGCAGCGGTTCCTCAAGCTTCAAAATATCTCCCTTCACAGG 1056
Db 1067 GTGGAAGAGATGTTTCATTGAGCTGATTCAAAGACTTCAAAATCCGACGAGTAGCTGG 1126
QY 1057 ATATTGCTCTTATTGAGATCTATCTTGAATGACTGACGCTGCAATATTC 1108
Db 1127 CCTCATGTCGTCATCGAGGTCTATCCATGAATCTTTGTGAACAAAAGGCC 1178

RESULT 14

US-09-938-842A-2582
; Sequence 2582, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2582
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2582

Query Match 8.6%; Score 100.2; DB 10; Length 1149;
Best Local Similarity 56.4%; Pred. No. 1.3e-16;
Matches 208; Conservative 0; Mismatches 158; Indels 3; Gaps 1;
QY 516 TCAATGAGGCAATGGCTTGATTC---TCAGATTTGAACCTTGGCGTTTAGAGATTGCA 572
Db 554 TCAATGAGGCAATGGCTTGATTCAGAGGGCGGTGTCACACGTGTAGCGGAGCTTGTC 613
QY 573 ATTGGGTCTTTGAGGAGCTGAATCCATTGTGATGTTGTGGTGGAACTGGAATCACAG 632
Db 614 ACGCTTTGTTGATGGCGTACATGATGTTGACGTAGAGGTGGTACGGGAGAGACGA 673
QY 633 CAAAGATTATCTGTAGGCTTTTCCTAAGCTGAAATGCATGGTGTGGAACGTCCAAATG 692
Db 674 TGGGATGCTTGTGAAGAGTTTCCTTGGATCAAGGATTTAATTGTATCTTCCTCATG 733
QY 693 TTGTGGAATTTGTGAGGAGCAACAAATTTGATTTGTTGGTGGGCAATGTTTAAAT 752
Db 734 TCATTGAAGTTGCTGAAAGTCTTGACCGGTGTGAGAAATGTTGAGGGCGATATGTTGATT 793
QY 753 GCATCCCCAAGGCTGATGCAAGTCTGCTTAAGTTGGTTTACATAATTTGAATGACAAAG 812
Db 794 CTATTCGGGCTGCGACGCCATTTTCATCAAGTGGGTGTTACACGATTGGGGAGACAAAG 853

QY 813 ATTGCATGAAGATATTAGAAAATTGTAAGAAGCTATTTTCAGGTGAAAGCAAAACAGGAA 872
Db 854 ATTGCATGAAGATATTGAAGAAATTGCAAGAGCGGTCCCTCCAAATATCGGAAAAGTGT 913
QY 873 AAGTAGTTG 881
Db 914 TGATAGTGG 922

RESULT 15

US-09-796-256A-5
; Sequence 5, Application US/09796256A
; Patent No. US20020078477A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Carraway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617/c-3532.0
; CURRENT APPLICATION NUMBER: US/09/796,256A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US60/033381
; PRIOR FILING DATE: 1996-12-16
; PRIOR APPLICATION NUMBER: 08/991677
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1170)
US-09-796-256A-5

Query Match 8.2%; Score 94.6; DB 9; Length 1380;
Best Local Similarity 50.1%; Pred. No. 4.9e-15;
Matches 325; Conservative 0; Mismatches 309; Indels 15; Gaps 3;
QY 404 TGGAACAGTTGAAGAGGTGGGTTTCATGAGGAAGATCTCACAGTATTTGAGGTCTCCTTA 463
Db 490 TGGTACCACCTTGACCGAGCGAGTTCCTTGAAGGTGGAATTCATTAACAGGCGCTATGGA 549
QY 464 GGAACACCTTCTGGGACCTTTATCAATAAGACCCCTGCATATAACAAGTCATTCATGAG 523
Db 550 ATGACAGCATTTGAGTACCATGGC---ACCGATCCAGATTCACACACAGTTTTCACAAAT 606
QY 524 GCAATGGCTTGTGATTTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAATTTGGGTCTTT 583
Db 607 GGAATCTCCAATCATTCGACCATTACCATGAAGAAATCTTTGAGACTTACAAGGGTTTC 666
QY 584 GAGGAGCTGGAATCCATTCGATTTGATGTTGGTGGAACTTGGAAATCACAGCAAAAGATTATC 643
Db 667 GAGGAGCTTGGATCTCTGCTGTGATGTTGGTGGCACTGGTGCACCACCTTAACATGATT 756
QY 644 TGTGAGGCTTTTCCCTTAAGCTGAAATGCAATGCTGTTTGGACGTTCCAAATGTTTGGAAAT 703
Db 727 ATGCTTAAATACCCCATGATCAAGGSCATTAACTTCGACTTCCTCATGTTATTGAGGAG 786
QY 704 TTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGACATGTTTAAATGCATCCCAAG 763
Db 787 GCTCCCTCCTATCCTGGTGTGGGCAATGTTGGTGGAGATATGTTGTTAGTGTTCCTCAAA 846
QY 764 GCTGATGCAAGTCTGCTTAAGTTGGTTTACATAATTTGAATGACAAACGATTGCATGAAG 823
Db 847 GGAGATGCCATTTTCATGAAGTGGATATGTCATGATTGGAGCGATGACACACTGCTTGAAG 906
QY 824 ATATTGAAAATTTGAAGAAGCTATTTTCAGGTGAAGCAAAACAGGAAAAGTAGTTGTC 893
Db 907 TTTTGAAGAAATGTTATGAAGCACTTCCA-----ACCAATGGGAAGGTGATCTCT 957

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QY 884 ATAGATACCTGTGATAAAGCAACAAAGATGAGCGCCCAAGTTACTGAACTAAAGTCCTT 943
Db || || || || || || || || || || || || || || || || || || || || ||
958 GCTGATGCACTCCCTCCCGTGGCGCCAGACGCAAGCCTCCCACTAAGGCACTGGTCCAT 1017
QY 944 ATGGATGTACACA---TGGCATGTATTATTAAATGGAAGAGAGAGAAAAGAAAGAGATTGG 1000
Db || || || || || || || || || || || || || || || || || || || || ||
1018 ATTGATGTATCATGTGTTGGCTCATAACCCAGGTGGGAAAGAGAGAACTGAGAGGAGTTT 1077
QY 1001 AAGAACTCTTTCATGGAAGCAGGGTTCCAAGCTACAAAATATCTCCCT 1049
Db || || || || || || || || || || || || || || || || || || || || ||
1078 GAGGCTTGGCCAAAGGGGGCTGGATTGAGGTTTCGAGTAGAGCCT 1126

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Search completed: November 10, 2003, 03:17:19
Job time : 463 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 23:36:19 ; Search time 2914 Seconds
(without alignments)

9675.083 Million cell updates/sec

Title: US-09-868-547-3

Perfect score: 1160

Sequence: 1 gttgtattatggtcttctt.....ataaaagtattcttggtt 1160

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estbta.*

2: em_esthum.*

3: em_estlin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	650.4	56.9	697	9 AW350290	AW350290 GM210008A
2	588	50.7	589	12 BM523459	BM523459 sam84a09.
3	557.8	48.1	561	13 BQ452916	BQ452916 sa093b08.
4	548	47.2	573	12 B1245401	B1245401 F1S1C9 Po

ALIGNMENTS

RESULT 1
AW350290/c
LOCUS :
DEFINITION
GM210008A10D3 Gm-r1021 Glycine max cDNA clone Gm-r1021-2837 3',
mRNA sequence.
ACCESSION
AW350290
VERSION
AW350290.1 GI:6848000
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 697)
AUTHORS
Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V.,
Erdelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.
TITLE
A Functional Genomics Program for Soybean (NSF 9872565)
JOURNAL
Unpublished
COMMENT
Other_ESTs: AW3507864
Contact: Vodkin, L.O., PI, A Functional Genomics Program for
Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147

5 493 42.5 494 9 AW3507864
6 456.2 39.3 852 10 BG588377
7 442.6 38.2 822 10 BG645368
8 439.2 37.9 569 12 BM188258
9 437.4 37.7 606 12 BM177364
10 417.8 36.0 788 13 BQ165419
11 415.8 35.8 693 14 CA921971
12 413 35.6 546 12 BM178815
13 410 35.3 826 13 BQ165418
14 405 34.9 625 9 AW733746
15 405 34.9 775 13 BQ165420
16 397.2 34.2 774 9 AW559420
17 390.6 33.7 742 9 AW267810
18 387 33.4 408 13 BU765089
19 385.8 33.3 503 10 BG511336
20 383.2 33.0 420 10 BE021456
21 379.6 32.7 718 13 BU091459
22 375.8 32.4 512 10 BG509454
23 364 31.4 551 9 AW309379
24 353.8 30.5 519 10 BG509170
25 348.8 30.1 668 13 BQ156708
26 348.8 30.1 746 14 CA783352
27 338 29.1 563 12 BM528698
28 330.8 28.5 639 10 BE999705
29 330.2 28.5 763 9 AW348354
30 329.6 28.4 643 10 BF48180
31 327.2 28.2 519 10 BE943072
32 327 28.2 327 9 AI441334
33 320.8 27.7 592 13 BU577747
34 318 27.4 634 10 BF650939
35 310.4 26.8 779 14 CB891286
36 309.6 26.7 496 13 BU549771
37 295 25.4 615 10 BG448331
38 290 25.0 305 13 BQ627748
39 287.4 24.8 577 9 AW559532
40 285.4 24.6 623 9 AW584374
41 284.4 24.5 577 9 AW585248
42 281 24.2 541 12 BI417247
43 280.8 24.2 546 9 AW507849
44 279.4 24.1 600 10 BF637366
45 269.2 23.2 591 13 BU764527

AW350290 697 bp mRNA linear EST 04-OCT-2000
GM210008A10D3 Gm-r1021 Glycine max cDNA clone Gm-r1021-2837 3',
mRNA sequence.
ACCESSION
AW350290
VERSION
AW350290.1 GI:6848000
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 697)
AUTHORS
Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V.,
Erdelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H.
TITLE
A Functional Genomics Program for Soybean (NSF 9872565)
JOURNAL
Unpublished
COMMENT
Other_ESTs: AW3507864
Contact: Vodkin, L.O., PI, A Functional Genomics Program for
Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147

445	Qy	AGTATTGAGTCTCCTTAGGAACACCTTCTCTGGACTTTATCAATAAAGACCCCTGCATA	504
697	Db	AGTATTGANNNNCNTTAGGAA-NNNNNNNNGGACNNNNNNCNTNAAAGACCCCTGCATA	639
505	Qy	TACAAAGTCATTCAATGAGGCAATGGCTTGATCTTCAGATCTGGAATTCGGCGCTTAG	564
638	Db	TACAAAGTCATTCAATGAGGCAATGGCTTNGATCTTCAGATCTGGAATTCGGCGCTTAG	579
565	Qy	AGATTGCCAATTGGTGCTTTGAGGCACTGGAAATCCATTGTGGATCTTGGTGGTGGAACTGG	624
578	Db	AGATTGCCAATTGGTGCTTTGAGGCACTGGAAATCCATTGTGGATCTTGGTGGTGGAACTGG	519
625	Qy	AATCAGCAAGAAAGATTATCTGTGAGGCTTTTCCCTAAAGCTGAAATGCATGGTGTGGAACG	684
518	Db	AATCAGCAAGAAAGATTATCTGTGAGGCTTTTCCCTNAGCTGAAATGCATGGTGTGGAACG	459
685	Qy	TCCAAATGTTGTGGAAAAATTCCTCAGGAAGCAACAATTTGCACATTTGTTGGTGGGACAT	744
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745	Qy	GTTTAAATGCATCCCAAGGCTGATGCAGTTCTCTGCTTAAGTTGGTTTTACATAAATTTGGAA	804
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338	Db	TGACAACGATTGCATGAAGATATTAGAAAAATTGAAGAAGCTATTTCACGGTGAAGCAAA	279

QY 625 AATCAGCAAGAAATATCTGTGAGGCTTTTCTTAAGCTGAATGATCATGTTGTGAAGC 684
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 QY 61 AATCAGCAAGAAATATCTGTGAGGCTTTTCTTAAGCTGAATGATCATGTTGTGAAGC 120
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 QY 685 TCCAAATGTTGGAAATTTGTCCAGGAGCAACATTTGACATTTGTTGGTGGGACAT 744
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 QY 121 TCCAAATGTTGGAAATTTGTCCAGGAGCAACATTTGACATTTGTTGGTGGGACAT 180
 QY 745 GTTAAATGATCCCAAGGCTGATGACGTTCTGCTTAAGTTGGTTTACATAATTTGAA 804
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 QY 181 GTTAAATGCTTTCCCAAGGCTGATGACGTTCTGCTTAAGTTGGTTTACATAATTTGAA 240
 QY 805 TGACACAGATTCGATGAAGATTTAGAAATTTGTAAGAGCTATTTCAGGTGCAAGCAA 864
 Db |||||
 QY 241 TGACACAGATTCGATGAAGATTTAGAAATTTGTAAGAGCTATTTCAGGTGCAAGCAA 300
 QY 865 AACAGGAAAGTAGTTGTCATAGATCTGTGATTAACGAAACAAAGATGACGCGCAAGT 924
 Db |||||
 QY 301 AACAGGAAAGTAGTTGTCATAGATCTGTGATTAACGAAACAAAGATGACGCGCAAGT 360
 QY 925 TACTGAATTAAGCTCCTTATGATGTACACATGGCATGTATTATTATGGAAGAGAGAG 984
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 QY 361 TACTGAATTAAGCTCCTTATGATGTACACATGGCATGTATTATTATGGAAGAGAGAG 420
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 QY 481 TCCCTTTCAGAGATTTGCTCTTATTGAGATCTTCTGTAATGACTGACGCTCAATA 1104
 QY 1105 TTCCATTTAGTAAATTTG 1125
 Db |||||
 QY 541 TTCCATTTAGTAAATTTG 561
 Db |||||

RESULT 4
 B1245401
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 DEFINITION
 B1245401
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 B1245401
 573 bp mRNA linear EST 30-DEC-2001
 Fis1C9 Forrest infected Subtraction Library Glycine max cDNA, mRNA
 sequence.
 B1245401
 GI:17998777
 EST.
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE
 1 (bases 1 to 573)
 Iqbal,M.J. and Lightfoot,D.A.
 Differentially expressed mRNA sequences identified by subtraction
 hybridization from soybean, Glycine max (L.) Merr. var. Forrest,
 roots in response to Fusarium solani f. sp. glycinae inoculation
 Unpublished
 Contact: Iqbal MJ and Lightfoot, DA
 Center of Excellence in Soybean Research, Teaching and Outreach
 Southern Illinois University at Carbondale
 Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415,
 USA
 Tel: 618 453-3121
 Fax: 618 453-7457
 Email: mjiqbal@siu.edu, ga4082@siu.edu
 Seq primer: M13 Forward.
 Location/Qualifiers
 1..573
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultiivar="Forrest"
 /db_xref="taxon:3847"
 /dev_stage="14 days after inoculation"

FEATURES
 source

/clone.lib="Forrest infected Subtraction Library"
 /note="Organ: Root; Vector: pGEM; Forrest roots were
 inoculated with Fusarium solani f. sp. glycinae and
 samples were collected after 14 days of inoculation. Total
 RNA was used for cDNA synthesis using SMART PCR cDNA
 synthesis kit (CLONTECH, CA). CLONTECH PCR-Select
 Subtraction system was used to enrich rare transcripts
 expressed in Forrest roots under inoculation by F. solani
 and cloned in pGEM vector. ESTs were sequenced using M13
 universal forward or reverse primer."
 BASE COUNT 169 a 116 c 119 g 169 t
 ORIGIN

Query Match 47.2%; Score 548; DB 12; Length 573;
 Best Local Similarity 100.0%; Pred. No. 9e-109;
 Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 26 GTTTGCTATTATGGCTTCTTCATTAAACAATGGCGTAAAGCAAGTAGAGATTTTCAAGG 85
 Db |||||
 QY 61 TCAAGCTCTCTGTGACAAACAATTTGCTTGGCTTCATAGATTCTTAAGTGTCTTAAATGAT 120
 Db |||||
 QY 86 TCAAGCTCTCTGTGACAAACAATTTGCTTGGCTTCATAGATTCTTAAGTGTCTTAAATGAT 145
 QY 121 GGTGAGCTTGACATACCGACATAATCCACAGCCATAGCCATGGCCAAACCCATTACTTT 180
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 QY 146 GGTGAGCTTGACATACCGACATAATCCACAGCCATAGCCATGGCCAAACCCATTACTTT 205
 QY 181 TTCAGAGTTGGTGTCAAATTTCTACAAGTCCCAACCACTAAACTCTCAGAGTGCAGAGCCT 240
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 QY 206 TTCAGAGTTGGTGTCAATTTCTACAAGTCCCAACCACTAAACTCTCAGAGTGCAGAGCCT 265
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 Db |||||
 QY 266 CATCGGTTATCTAGCACACAATGGAATCTTTGAGATAGTAAGAATCCATGACAACATAGA 325
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 Db |||||
 QY 326 AGCATATGCTCTCACTGCTTCAGAGTTACTTGTCAAAAGCAGTGCAGCTTAGCTTAGC 385
 QY 361 TCCAATGGTTGAGTATTTTCTTGAACCAAAATTTGCAAGGTGCATGGAACCAAGTTGAAGAG 420
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 QY 386 TCCAATGGTTGAGTATTTTCTTGAACCAAAATTTGCAAGGTGCATGGAACCAAGTTGAAGAG 445
 QY 421 GTGGGTTCAATGAGGAAGATCTCAGATTTTGGAGTCTCCTTAGGAACAACCTTTCTGGGA 480
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 QY 446 GTGGGTTCAATGAGGAAGATCTCAGATTTTGGAGTCTCCTTAGGAACAACCTTTCTGGGA 505
 QY 481 CTTTATCAATAAAGACCCCTGCATATAACAAGTCAATCAATCAGGCAATGGCTTGATTC 540
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 QY 506 CTTTATCAATAAAGACCCCTGCATATAACAAGTCAATCAATCAGGCAATGGCTTGATTC 565
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 QY 566 TCAGATGT 573
 Db |||||

RESULT 5
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 DEFINITION
 A1507864
 494 bp mRNA linear EST 28-NOV-2001
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 Gm-cl004-6344 5' similar to TR:022308 O22308 7-O-METHYLTRANSFERASE.
 [3] TR:022309 TR:022555 ; mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 A1507864
 GI:4405715
 EST.
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

1 (bases 1 to 494)

REFERENCE
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corryell,V., Khan,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,X., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson,R.

TITLE Public Soybean EST Project

JOURNAL Unpublished

COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert length: 1307 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 393
POLYA=No.

FEATURES
source Location/Qualifiers
1..494
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-6344"
/tissue_type="root"
/lab_hosts="XU10-Gold"
/clone_lib="Gm-cl004"
/notes="vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First- strand synthesis is performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGAACTAGTCTGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Corryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Corryell), Fax: 520-523-7500, email: paul.keim@na.u.edu, virginia.corryell@na.u.edu"

BASE COUNT 144 a 103 c 101 g 145 t 1 others

ORIGIN

Query Match 42.5%; Score 493; DB 9; Length 494;
Best Local Similarity 99.8%; Pred. No. 8.1e-97;
Matches 493; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGCGTCTCTCATTAACAATGGCCGTAAGCAAGATGAGATTTTCAAGGTCACAGCTCTCT 71

Db 1 TGCGTCTCTCATTAACAATGGCCGTAAGCAAGATGAGATTTTCAAGGTCACAGCTCTCT 60

OY 72 TGTACAAACATTGGCTTGGCTTCATGATCTTCAAGTGTCTPAAATGATGGTTGACGTTG 131

XhoI; At the trifoliate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this period, they were fertilized twice weekly with 1/2 Hoaglands solutions containing 20mM potassium phosphate. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

```
BASE COUNT      268 a   121 c   189 g   274 t
ORIGIN
Query Match      39.3%; Score 456.2; DB 10; Length 852;
Best Local Similarity 73.8%; Pred. No. 9.2e-89;
Matches 613; Conservative 0; Mismatches 203; Indels 15; Gaps 2;
QY 106 GTGCTAAATGGATGGTTGAGCTTGACATCCCGACATAATCCACAGCATAGCCATGG 165
Db 28 GTCTCTTAATGGTCAGTTGAATGGACATACCAACTATTATCTAC-----AATCATGG 81
QY 166 CCAACCCATTACTTTTTCAGAGTTGGTGCATTAAGTCAAGTCCCAACCACTAAACTCG 225
Db 82 CAACCAATTAATCTCTTCAAACTTAGTTTCAATTTCTCAAAATTCATCAACCAAGTCGA 141
QY 226 TCAGTGCAGAGCCATCATGCGTTATCTAGCACACATGATCTTTTGATAGTAAGAAAT 285
Db 142 TAACGTGCGAGGTCTATCGCGTCTCCTTGCACCAATGATCTTTTGATAGTAAGCAA 201
QY 286 CCATG-----ACAACATAGAACATATGCTCTCACTGTGCTTCCAGAGTTACTTGT 336
Db 202 TCAAGAAATGGAAATGAAGAAGAGCTATGCTCTCACAGTACTTCCAGAGCTTCTTGT 261
QY 337 CAAAGCAGTGAAGCTTAGTCTCCAAATGGTTCAGTATTTTCTGTGAACCAATGTCFA 396
Db 262 TAAAGGGAAGTGAAGCTTTGTTAGTCCCAATGGTTCAGTGTGTTCTGTATCTCTAAATTTAA 321
QY 397 AGGTGCATGGACCAAGTTGAAGAGTGGTTCATGAGGAAGATCTCACAGTATTTGAGGT 456
Db 322 TGTTCATTTCAATATTTCAAGAAGTGGATTTATGAGGAAGATCTCACCCCTTTGTGTAC 381
QY 457 CTCCTTAGGAACACCTTTCTGGGACTTTTATCAATAAAGACCTGCTATATAACAGTCAAT 516
Db 382 CTCCTTAGGATGTGATTTATGGAGTTTCTTAACAAATAATCTGATATATAGATCTTT 441
QY 517 CAATGAGCAATGCTTGTGATCTTCAGATGTGAATGCGTTGCGTTAGAGATTCGAATG 576
Db 442 CAATGATGCTATGGCTAGTGTATTCAAAATGATTAATTTGGCAATGGAAGATTGCAATTT 501
QY 577 GGTCTTTGAGGACTGGGAATCCATTTGCGATGTTGGTGTGGAATGGAATCAGACGAA 636
Db 502 TGTGTTGAGGGTTGGATTCAATTTGUGATGTTGGTGTGGAATGGAACCACTGGTAA 561
QY 637 GATTATCTGAGGCTTTTCTTAAGTGAATGCAATGCTGTTGGAACGTCCTCAATTTGT 696
Db 562 GATTATTTGTGAGACATATCCTAAGTTCAGATGCTGTTGTTTGTATCTCCAAAGTTGT 621
QY 697 GGAATTTTGTGAGGACCAATTTGACATTTGTTGGTGGGACATGTTTAAATGCAAT 756
Db 622 AGAATTTTATTTGTGAAGTAAATTTGACATATGTCGGTGGGACATGTTTATATCTGT 681
QY 757 CCCAAGGCTGATGAGTTCTGTTAAGTGTGTTTATACATATTTGGAATGACAGATTG 816
Db 682 TCCTAAGCTGATGAGTTCTGTTTAAAGTGAATTTTATCATTTGGACGGATAGGATTG 741
QY 817 CATGAAGATATTAGAAAATTTGAAGAAGCTATTTTCAGGTGAAAGCAAAACAGGAAAGT 876
Db 742 CATAAAGATATTGAAGAAATTTGAAGAAGCTGTTTACAACTGAGGGGAAAGAGGAAAGT 801
QY 877 AGTTGCTATAGACTGTGATAACGAAACAAAGATGAGCGCCCAAGTTTAC 927
Db 802 GATTGTGATAGACATGGTAAATAATGAAAGGAAGGAGAGACGAACTTAC 852
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RESULT 7
BG645368
LOCUS
DEFINITION
EST506987 KV3 Medicago truncatula cDNA clone PKV3-46C11 5' end,
mRNA sequence.
ACCSSION
BG645368
VERSION
BG645368.1 GI:13780480
KEYWORDS
EST,
SOURCE
Medicago truncatula (barrel medic)
ORGANISM

REFERENCE
1 (bases 1 to 822)
AUTHORS
VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman
.C.L., Craven,M.B., Cho,J. and Fraser,C.M.
TITLE
ESTs from roots of Medicago truncatula 72 h after Rhizobium
inoculation, 2001
JOURNAL
Unpublished
COMMENT
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biosci. Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbbs.umn.edu
M393775e TIGR sequence name: MTECA18TK More information is
available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtg gat CC).
Location/Qualifiers

FEATURES
source

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/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XL0LR"
/clone_lib="KV3"
/notes="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
BASE COUNT 250 a 124 c 169 g 279 t
ORIGIN

Query Match 38.2%; Score 442.6; DB 10; Length 822;
Best Local Similarity 74.2%; Pred. No. 8.3e-86;
Matches 605; Conservative 0; Mismatches 194; Indels 16; Gaps 3;

QY 18 CTTCAATTAACAATGGCGGTAAAGCAAGTGAAGATTTTCAAGGTCAAGCTCTCTTGACA 77
Db 15 CTTCTTCAATAAATAACCGTAAGCAAGTGAATTTTCAAGCAAGCTCTATTATACA 74
QY 78 AACATTTGCTGGTTCATAGATTCTAAGTGTCTTAAATGATGTTGAGCTTGACATAC 137
Db 75 AAAACATGATGTTGTTTTCATAGATTCCTTCTTAAATGCTCAGTTGAAATGGACATAC 134
QY 138 CCGACATAATCCACAGCCATAGCCATGGCCAACTTCTTTCAGAGTTCGTTGCTCAA 197
Db 135 CAACATTAATCTAC-----AATCATGGCAACCAATTTCTTTCAAACTTAGTTTCAA 188
QY 198 TTCTACAAGTCCCAACCACTAAAACTCGTCAGGTGACAGCCCTCATGCGTTATCTAGCAC 257
Db 189 TTCTTCAAAATTCATCAACCAAGTCGATAACGTCGAGCGGTCTCATGCGTCTCTTCTGCAC 248

QY 633 CAAAGATTATCTGTGAGGCTTTTCTAAGCTGAATGATGTTGTTGGAACTGCAAAATG 692
 Db 418 CCAAGATTATCTGTGAGGCTTTTCTAAGCTGAATGATGTTGTTGGAACTGCAAAATG 477
 QY 693 TTGTGAAATTTGTGAGGCAACAAATTTGACATTTTGTGTTGGGACATGTTTAAAT 752
 Db 478 TTGTGAGAACTTGTGAGGCAACAAATTTGACATTTTGTGTTGGGACATGTTTCAAT 537
 QY 753 GCATCCCAAGCTGATGAGTCTGCTTAAG 784
 Db 538 CTATTTCCCAAGGCTGTGCAGTCTATTTAAG 569

RESULT 9
 BM177364 606 bp mRNA linear EST 06-DEC-2001
 DEFINITION Sa980D09.v1 Gm-cl074 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl074-2873 5' similar to TR:022555 O22555 O-METHYLTRANSFERASE. [2
] TR:022308 ;, mRNA sequence.

ACCESSION BM177364
 VERSION BM177364.1 GI:17400582
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 606)
 Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 ,R., Waterston,R. and Wilson,R.
 Public Soybean EST Project

TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact: cu@resgen.com web site:
 www.resgen.com

Seq primer: -40RP from Gibco
 High quality sequence stop: 442.

FEATURES
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 XhoI; The cDNA library was constructed from mRNA isolated
 from 9-11 day old seedlings that were induced for HR
 (hypersensitive response) by vacuum infiltrating plant
 tissue with Pseudomonas syringae pv. glycinea carrying the
 avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
 unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36
 and 53 hrs after inoculation and their mRNA pooled equally
 for cDNA construction. The library was prepared using the
 Stratagene pluscript II SK(+) library construction kit.
 Complementary DNA was synthesized from mRNA using a primer

consisting of a poly(dT) sequence with an XhoI restriction
 site. EcoRI adaptors were ligated to the blunt-ended cDNA
 fragments followed by XhoI digestion. The cDNA insert is
 protected from XhoI digestion via methylation during first
 strand synthesis. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into E.coli ElectroMax DH10B host cells. Plant
 care, inoculations, and library construction were
 performed by Steve Clough (Lila Vodkin lab, University of
 Illinois)." 178 a 122 c 119 g 187 t

Query Match 37.7%; Score 437.4; DB 12; Length 606;
 Best Local Similarity 85.6%; Pred. No. 1.1e-84;
 Matches 525; Conservative 0; Mismatches 76; Indels 12; Gaps 3;
 QY 1 GTTTGCTATTATGCTTCTTTCATTAACAATGGCCGTAAGCAAGTGAGATTTTCAAGG 60
 Db 6 GTTTGCAATTATGGCTTCTTC---AATCAATGGCCGTAATGAAAGTGAGATCTTTCAAGG 62
 QY 61 TCAAGCTCTCTGTGACAAACATTTGGCTTCATAGATTTCTAAGTGTCTAAATGCAT 120
 Db 63 TCAACTCTCTGTGACAAACATTTGTATGCTTCATAGATCTCTATGTCTCAATGCAT 122
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 Db 123 TGTGAGCTTGGAAATACAGACATAATCCAC-----AACCATGGCCCAACCCATTACTCT 176
 QY 181 TTCAGAGTGGTGTCATTTCTACAAGTCCCAACCACTAAAACCTCGTCAGGTGCAGAGCT 240
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 QY 361 TCCAAATGGTTGAGTATTTCTTGAAACCAATTTGTCAGGTGTCATGGACCAAGTTGAAGAG 420
 Db 354 TCCAAATGATTTGAGTTGTTCTTGACCCCACTTTGTCAAAATTCATTCATCAATTGAAAAA 413
 QY 421 GTGGGTTTCATGAGGAAGATCTCAAGTATTTGAGGTCTCCTTAGGAACACCTTTCTGGGA 480
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 QY 481 CTTTATCAATAAAGACCCCTGCAATATAACAAGTCATTCAATGAGGCAATGGCTTGTGATTC 540
 Db 474 CTTTCTTAATAAAGACCCCTGCAATATAACAAGTCATTCAATGAGGCAATGGCTTGTGATTC 533
 QY 541 TCAGATGTTGAACCTTGGCGTTTGAAGATTCGATTTGGGTCTTTGAGGAGCTGGAATCCAT 600
 Db 534 TCAGATGATGAACCTTGGCGTTTGAAGATTCGATTTGGGTCTTTCAAGGAGCTGGAATTCAT 593
 QY 601 TGTGATGTTGGT 613
 Db 594 TGTGATGTTGGT 606

RESULT 10
 BQ165419

LOCUS BQ165419

DEFINITION

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

BQ165419 788 bp mRNA linear EST 25-APR-2002
 BQ165419 KVKC Medicago truncatula cDNA clone PKVKC-9A5, mRNA
 sequence.

BQ165419.1 GI:20307786

EST.

Medicago truncatula (barrel medic)

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 788)

VandenBosch, K., Endre, G., Silverstein, K, Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and re-arrayed from various libraries

JOURNAL COMMENT

Unpublished
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738

Email: kvandenb@cs.umn.edu
TIGR sequence name: MTN0105TK Alias Clone name: DSIR-19L16 More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtg GAT CC).

FEATURES source

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/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-aseII helper phage and propagated in XL0LR cells."

BASE COUNT ORIGIN

Query Match 36.0%; Score 417.8; DB 13; Length 788;
Best Local Similarity 73.7%; Pred. No. 2e-80;
Matches 57; Conservative 0; Mismatches 192; Indels 14; Gaps 3;

QY 33 GCCGTAAGCAAGTGTGATTTTCAAGTCAAGCTCTTGTCAAAACATTGCTGCT 92
DB 18 GGCAGAAACACAGTGAATTTTCAAGGCACAGCTTTATTATACAAACATATTTCCT 77
QY 93 TCATAGATTTCAAGTGTCTAAATGGATGGTTGAGCTTGACATACCCGACATATCCACA 152
DB 78 TCATAGATTTCCATGCTCTTAAATGGGCTGTGAATGAACATACCAATATTATTCAC- 136
QY 153 GCCATGCCATGCCACCACTTACTTTTTCAGATGGTGGTCAATCTCAAGTCCAC 212
DB 137 -----AATCATGGCAACCAATTTTCACTTTCAAAATTTAGTTTCAAGTTCCAT 191
QY 213 CAACATAAACTCGTCAGGTGCAGAGCCTCATCGCTTATCTAGCACAAATGGATTTCTTG 272
DB 192 CGTCGAAATAGGTAACTGTCGGGCTCTCATGCTTACCTCGCCACACAGGATTTCTTG 251
QY 273 AGATAGTAAGATCCATGACAAATAGCATAGCATATGCTCTCACTGCTTCAGAGTTAC 332
DB 252 AGATAATTAACAAAAGA-----AGAGTCTTATGCTCTCACTGTTGCTTCAGAGTTC 305
QY 333 TTGTCAAAGCAGTGGCTTAGTTAGTCTCAATGGTTGAGTATTTTCTTGAACCAAT 392
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QY 393 GTCAAGGTGATGGAACCAAGTTGAAGAGGTGGTTTCATGAGGAGAGATCTCACAGTATTG 452
DB 366 TTTCGGGTTGATCATGAGCTGAAGAAATGGATTTATGAGGAAGATCTTACACTCTTTG 425

QY 453 AGGTCTCTCTTAGGAACACCTTTCTGGGACTTTATCAATAAGACCCCTCATATAACAAGT 512
DB 426 GTGTTACTTTAGGCTCTGGTTTTTGGGATTTTCTTGATAAAATCCTGAAATATATAGAT 485
QY 513 CATTCAATAGGCAATGGCTTGTGATTCTCAGATGTTTGAACCTTGGCGTTAGAGATTGCA 572
DB 486 CATTTAATGATGCAATGGCTAGTCATTCTAAATGATAAACTTGGCATTGAGAGATTGTG 545
QY 573 ATTGGGCTTTGAGGGAAGTCCATTCATGTTGGATGTTGGTGGGAACATGCAATCAG 632
DB 546 ATTTTGGTTTGTGAGTGGATTCGAATCAATTTGGGATGTTGGTGGGAATGGAACCATG 605
QY 633 CAAAGATTATCTGTGAGGCTTTTCTTAAGCTGAAATGCATGGTGTGGAACGTCCTCAATG 692
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DB 666 TTGTAGAGAACTTATCTGGAAGCAATAATTGACTTTTATGTTGGTGGGACATGTTTAC 725
QY 751 ATGCATCCCAAGGCTGATGCAGTTCCTGCTTAAGTTGGTTTACATATTTGGAATGACAA 810
DB 726 ATCTATTCCTAATGCTGATGCAGCTTTGCTTAAGTATATTTTACATAATTGGACTGATA 785
QY 811 CGA 813
DB 786 GGA 788

RESULT 11 CA921971/c

LOCUS CA921971 693 bp mRNA linear EST 09-MAY-2003
DEFINITION EST639689 MTUS Medicago truncatula cDNA clone MTUS-46H12, mRNA sequence.
ACCESSION CA921971
VERSION CA921971.1 GI:27408901
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 693)
AUTHORS VandenBosch, K., Endre, G., Silverstein, K, Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
TITLE The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries

JOURNAL COMMENT

Unpublished
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cs.umn.edu
Alias Clone pDSIR-19L16
TIGR sequence name: MTUS961V
More information is available at: www.medicago.org
Seq primer: (gta Ata Cga Ctc Act Ata ggg C).

FEATURES source

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/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA

was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT	240 a	147 c	79 g	227 t
ORIGIN				
Query Match	35.8%; Score 415.8; DB 14; Length 693;			
Best Local Similarity	77.5%; Pred. No. 5.4e-80;			
Matches 517;	Conservative 0; Mismatches 147; Indels 3; Gaps 1;			
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Db	693	TTTTGGATTTCTTGATAAAATCTCGAATAATAATAGATCATTTAATGATGCAATGGCTA	634	
QY	534	GTGATTCACAGATTTGAATTTGGCGTTTAGAGATTGCAATTTGGTCTTTGAGGACTGG	593	
Db	633	GTGATTCATAATGATAACITGGCATTGAGAGATTGTGATTTCTGTTGATGATTGG	574	
QY	594	AATCCATTTGTGATTTGTGTGGTGAACCTGGGAATCACAGCAAGATTTATCTGTGAGGCTT	653	
Db	573	AATCAATTTGTGATTTGTGTGGTGGAAATGGACCACTGGTAAATTTATTTGTGAGACTT	514	
QY	654	TTCTTAAGCTGAAATGCAATGGTGTGGAACTGCCAAATGTTGTGGAAATTTGTGAGAA	713	
Db	513	TTCTTAAGCTGAAATGCAATGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	454	
QY	714	GCAACAATTTGACATTTCTGTGGGGGACATGTTTAAATGATNATCCCAAGGCTGATGAG	773	
Db	453	GCAATAATTTGACATTTCTGTGGGGGACATGTTTCAATCTATTTCTTAATGCTGATGAG	394	
QY	774	TTCTGCTTAAGTTGTTTATACATTAATGCAATGCAACGATTCGATGAGATATTAGAA	833	
Db	393	TTTTCCTTAAGTATATTTCATTAATTTGACATGATGAGATTCGCAAGGATCTGAAGA	334	
QY	834	ATTGTAAGAGCTATTTTCAGTGAAGCAACAAACAGGAAAGTAGTTGTCATAGATCTG	893	
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Db	273	TCATAAATGAAAGAAAGATGAGAAATCAAGTTACTTCAAAATTAAGCTCTTTGAGATGAA	214	
QY	954	ACATGGCATGTATTATTATGAAAGAGAGAGAAAGAGAGATGGAAGAACTCTTCA	1013	
Db	213	ACATGGCTTG---TCTTAATGGAAGAGAGAAATGAGAAAGATGGAAGAACTCTTCA	157	
QY	1014	TGGAAGCAGGTTCCAAAGCTTACAAATATCTCCCTTCACAGGATATTGTCTCTTATTG	1073	
Db	156	TAGAAGCTGGTTTCCAGACTATAAGATATCTCCTTTGACTGGATTTTGTCTCTTATTG	97	
QY	1074	AGATCTATCCTTGAATAGTACGCTGCATATTCATTTAGTATTAAATTTGCAATGTTAT	1133	
Db	96	AGATCTATCCTTGAATAGTACGCTGCATATTCATTTAGTATTAAATTTGCAATGTTAT	37	
QY	1134	CAATPAA 1140		
Db	36	AAAGATA 30		
RESULT 12				
BM178815				
LOCUS	546 bp mRNA linear EST 06-DEC-2001			
DEFINITION	sa359h07.v1 Gm-cl072 Glycine max cDNA clone SOYBEAN CLONE ID:			
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] TR:022308 ;, mRNA sequence.			
ACCESSION	BM178815			
VERSION	BM178815.1 GI:17402033			
KEYWORDS	EST.			
SOURCE	Glycine max (soybean)			
ORGANISM	Glycine max			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 546)

Shoemaker, R., Keim, P., Vodkin, L., Expelding, J., Corvett, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R., and Wilson, R.

Public Soybean EST Project

Unpublished

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

Seg primer: -40RP from Gibco

High quality sequence stop: 421.

Location/Qualifiers

1..546

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-cl072-4190"

/tissue_type="seedlings induced for symptoms of SDS

(Sudden Death Syndrome) disease"

/dev_stage="2-3 weeks old"

/lab_host="DH10B"

/clone_lib="Gm-cl072"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; The cDNA library was constructed from mRNA isolated

from 2-3 week old seedlings that were induced for symptoms

of SDS (Sudden Death Syndrome) disease by the

translocation of culture filtrate of Fusarium solani f.

sp. Glycines (Plant Cell Report 18:375-380). Cultivar PI

567374 is partially resistant to the disease SDS. Plant

tissue (expanded leaves, folded leaves, and new shoots)

were collected at 1, 6, 24, and 48 hrs. after inoculation

and their mRNA pooled equally for cDNA construction. The

library was prepared using the Stratagene pBluescript II

SK(+) library construction kit. Complementary DNA was

synthesized from mRNA using a primer consisting of a

poly(AT) sequence with an XhoI restriction site. EcoRI

adaptors were ligated to the blunt-ended cDNA fragments

followed by XhoI digestion. The cDNA insert is protected

from XhoI digestion via methylation during first strand

synthesis. The cDNA fragments were directionally cloned

into the EcoRI-XhoI restriction site of the pBluescript

vector. The ligated cDNA fragments were transformed into

E.coli ElectroMax DH10B host cells. Plants were inoculated

by Shuxian Li (Glen Hartman lab, University of Illinois).

Library was constructed by Steve Clough (Lila Vodkin lab,

University of Illinois)."

BASE COUNT 165 a 101 c 113 g 167 t

Query Match 35.6%; Score 413; DB 12; Length 546;

Best Local Similarity 85.8%; Pred. No. 2.1e-79;

Matches 471; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY 173 ATTACTTTTCAGAGTTGGTGTCAATCTACAGTCCCACTAAACTCTGAGGTG 232

Db 1 ATTACTCTTCTGAGTTGGTGTCAATCTACAAATTCACCAAGTAAAGTTAGTCAAGTG 60

QY 233 CAGAGCTCATGCGTTATCTTAGCACAAATGGATCTTTGAGATAGTAGAATCCATGAC 292


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Db 121 AA--AGAAAGCATATGCTCTCACTGCTGCTTCCAGAGTACTTGTCAAAGCAGTGTGAGCTT 177
QY 393 AGTTTACGCTCCAAATGGTTGAGTATTTCTTGAACCAAAATGTCAAGGTGATGGAACACAG 412
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QY 413 TTGAAGAGGTGGTTTCATGAGGAAGATCTCAGAGTATTTGAGGTCTCTTGAAGAACACT 472
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QY 473 TTCTGGGACTTTTATCAATAAAGACCTTGATATAAAGTCAATTAAGTCAATTAAGTCAAT 532
Db 298 TTCTGGGACTTTTAAATAAAGACCTTGATATAAAGTCAATTAAGTCAATTAAGTCAAT 357
QY 533 TGTGATTTCTCAGATGTTGAACCTTGGGTTTGAAGTATGAAGTGAAGTGAAGTGAAGTGA 592
Db 398 AGTGATTTCTCAGATGATGAACCTTGGGTTTGAAGTATGAAGTGAAGTGAAGTGAAGTGA 417
QY 593 GAATCCATTTGAGATTTGGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 652
Db 418 GAATTCATTTGAGATTTGGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 477
QY 653 TTCTCTAAGCTGAATGATGCTGTTGGAACCTGCAATTAAGTGAAGTGAAGTGAAGTGAAG 712
Db 478 TTCTCTAAGCTGAATGATGCTGTTGGAACCTGCAATTAAGTGAAGTGAAGTGAAGTGAAG 537
QY 713 AGCAACAAT 721
Db 538 AGCAACAAT 546
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RESULT 13
LOCUS BQ165418
DEFINITION EST611275 KVRC Medicago truncatula cDNA clone pKVC-9A4, mRNA
ACCESSION BQ165418
VERSION BQ165418.1 GI:20307784
KEYWORDS EST
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 826)
VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,
Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and
re-arrayed from various libraries
Unpublished
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbosch@umn.edu
TIGR sequence name: MTN104TK Alias Clone name: DSIR-19C17 More
information is available at: www.medicago.org
Seq primer: SKmod (CTA gaa cta gta gat cc)
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
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/tissue_type="mixed tissues"
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/dev_stage="various stages"
/lab_host="XLOLR"
/clone_lib="KVRC"
/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
BASE COUNT 253 a 127 c 164 g 282 t
ORIGIN
Query Match 35.3%; Score 410; DB 13; Length 826;
Best Local Similarity 72.3%; Pred. No. 1e-78;
Matches 581; Conservative 0; Mismatches 205; Indels 18; Gaps 3;
QY 2 TTTCGATTTATGAGTCTTCTTCAATAAAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 61
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QY 122 GTTCGAGCTTTGACATACCGGACATATCCACAGCATAGCCATGCCAAGTGAAGTGAAGTGAAGT 181
Db 149 GTTCGAAATGACATACCAACTATTATCTAC-----AATCATGGCAACCAACTTACTCTT 202
QY 182 TCAGAGTTGGTGTCAATTTCTCAAGTCCCAACTAAACTCTGTCAGGTGACAGAGCTC 241
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Db 263 ATGCGTCTCTCTGACACAAATGGATTTCTTTGAGATAGTAAGATCCATGAGAAAT 322
QY 293 AACATAGAAGCATATGCTCTCACTGCTGCTTCCAGAGTACTTGTCAAAGCAGTGTGAGCTT 352
Db 323 GAAGAAGAGCTTATGCTCTCAGAGTACTTTCAGAGCTTCTTTGTAAGGGAGCTGAATTT 382
QY 393 AGTTTACGCTCCAAATGGTTGAGTATTTCTTTGAACCAAAATGTCAAGGTGACGAACACAG 412
Db 383 TGTTCAGCTCCAAATGGTTGAGTGTGTTGATCTTCAATTTTAAATTTCAATTTCAAT 442
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QY 473 TTCTGGGACTTTTATCAATAAAGACCTTGCAATATAAAGTCAATTAAGTGAAGTGAAGTGAAGT 532
Db 503 TTATGGGAGTTTCTTACAAATAATCCGATATTAATAGATTTGTTCAATGATGCTATGGCT 562
QY 533 TGTGATTTCTCAGATGTTGAACCTTGGCGTTTGAAGATTCGAATTTGGTCTTTGAGGAGCTG 592
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Db 743 AGTAACAATTTGACATTTATGCTGGTGGGACATGTTCAATCTTGTTCCTAAGCTGAT 802
QY 770 GCAGTCTCTGCTTAAGTTGGTTTAA 793
Db 803 GCAGTCTCTGCTTAAGTGGATTTTA 826
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Db	125	AACTTGGTCTTTTGAGGACTGGAAATCCATTTGTGATTTGGTGGTGAACCTGGAATCAC	184
Qy	632	GCAAAATATATCTGTGAGGCTTTTCCTAAGCTGAAATGATGCTGTTTGGAACTGCCAAAT	691
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Qy	692	GTTTGTGGAAAAATTTGTTCAGGAAGCAACAATTTGACATTTTGTGGTGGGACATGTTTTAA	751
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Qy	812	GATTTGCATGAAGATATTAGAAAAATTTAAAGAGACTAT--TTTCAGGTGAAAGCAAAACA	868
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Qy	929	GAACTAAAGCTCTTATGAGTGTACATCGCATGTATTATTAAATGAAAGAGAGAAAA	988
Db	485	GAACTAAAGCTGTTTGTGATGTAGCCATGCGATGCTATTATATGCAAGAGAGAGAT	544
Qy	989	GAGAAGATTTGGAAGAAACTTCTTCATGGAAGCGGGTTCGAAGCTACAAAATATCTCCC	1048
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Qy	1049	TTCACAGGATATTGTCTCTT	1069
Db	605	CTGACCGGCTCTGTCTCTT	625
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RESULT 15			
BQ165420/c			
LOCUS	BQ165420	775 bp	mRNA linear EST 25-APR-2002
DEFINITION	EST611277 KVKC Medicago truncatula cDNA clone pKVKC-9A5,	mRNA	
ACCESSION	BQ165420	sequence.	
VERSION	BQ165420.1	GI:20307788	
KEYWORDS	EST.		
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REFERENCE	1. (bases 1 to 775) Vanden Bosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Uterback, T., Cheung, F. and Fraser, C.M. The Medicago truncatula 'kiloclone' set; ESTs selected and re-arrayed from various libraries		
JOURNAL	Unpublished		
COMMENT	Contact: Vanden Bosch K Department of Plant Biology University of Minnesota 220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA Tel: 612 624 2755 Fax: 612 625 1738 Email: kvandenbos@bs.umn.edu TIGR sequence name: MTN105TV Alias Clone name: DSIR-19L16 More information is available at: www.medicago.org Seq primer: (gtA AtA CpA CtC Act AtA ggg C).		
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/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
BASE COUNT      272 a      158 c      90 g      255 t
ORIGIN

Query Match      34.9%; Score 405; DB 13; Length 775;
Best Local Similarity 77.6%; Pred. No. 1.2e-77;
Matches 516; Conservative 0; Mismatches 145; Indels 4; Gaps 2;

QY 477 GGGACCTTTATCAATAAAGCCCTGTCATATAACAAGTCATTCAATGAGGCAATGGCTTGTG 536
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QY 715 ATTCTAAATTGATAAATCGCATTTGAGAGATTGTGATTTTGTGTTGATGATGGAT 656
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QY 655 CAATTGTGATCTTGGTGTGGAATGGAACCACTGGGTAAATTTATTTGTGAGACTTTT 596
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QY 896 ATAAAGCAAAACAAGATGAGCGCCAAAGTTACTGAACCTAAAGCTCCTTATGGATGTACAC 955
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QY 178 ATCTATCCATAAACAATTTTGTATTGATCCATCATGCTCCTTATGCTGCTATAA 119
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Db ||| |||
QY 118 AGATA 114
Db ||| |||

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